

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2004, 19:12:49 ; Search time 2247 Seconds  
(without alignments)  
5426.840 Million cell updates/sec

Title: US-09-830-228-51

Perfect score: 2487

Sequence: 1 ATTATTATACAGAAACCTT.....TTAAGACACTTTGAAGA 2487

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	229.6	9.2	1300	17	US-10-668-749A-1
2	175.6	7.1	6668	15	Sequence 1, Appli
3	167	6.7	1204	17	Sequence 1670, Ap
4	161.2	6.5	6292	13	Sequence 77858, A
5	157	6.3	803	17	Sequence 461, App
6	154.2	6.2	14006	15	Sequence 72176, A
7	154	6.2	627	17	Sequence 1931, Ap
8	152.8	6.1	3673778	15	Sequence 9336, Ap
9	150.2	6.0	7442	13	Sequence 2, Appli
10	148.2	6.0	2520	17	Sequence 409, App
11	147	5.9	6767	13	Sequence 205, App
12	144.2	5.8	9539	15	Sequence 330, App
13	144.2	5.8	9539	15	Sequence 52, Appl
14	144	5.8	6334	15	Sequence 54, Appl
					Sequence 1186, Ap

C 15	141.2	5.7	34769	13	US-10-221-714A-501	Sequence 501, App
C 16	141	5.7	8079	17	US-10-240-589C-122	Sequence 122, App
C 17	140.4	5.6	31124	13	US-10-087-192-463	Sequence 463, App
C 18	139.8	5.6	529	9	US-09-983-965-2103	Sequence 2109, Ap
C 19	138.8	5.6	16033	15	US-10-311-455-1377	Sequence 1377, Ap
C 20	138.6	5.6	868	17	US-10-437-963-42302	Sequence 42302, A
C 21	137.8	5.5	9964	15	US-10-311-455-71	Sequence 71, Appl
C 22	136.4	5.5	3673778	15	US-10-312-841-1	Sequence 1, Appli
C 23	135	5.4	1214	13	US-10-424-599-102083	Sequence 102083,
C 24	134.4	5.4	5493	13	US-10-221-613-349	Sequence 349, App
C 25	133.2	5.4	7571	15	US-10-311-455-500	Sequence 500, App
C 26	132.8	5.3	522	14	US-10-101-487-71	Sequence 71, Appl
C 27	132.8	5.3	530	14	US-10-101-487-73	Sequence 69, Appl
C 28	132.8	5.3	554	14	US-10-101-487-106	Sequence 106, App
C 29	132.8	5.3	554	14	US-10-101-487-106	Sequence 1692, Ap
C 30	132.6	5.3	17934	15	US-10-311-455-1692	Sequence 9573, Ap
C 31	132	5.3	447	17	US-10-021-323-9573	Sequence 204, App
C 32	131.6	5.3	3505	17	US-10-389-566-204	Sequence 240, App
C 33	131.2	5.3	6419	15	US-10-311-455-240	Sequence 3400, Ap
C 34	130	5.2	446	9	US-09-960-352-3400	Sequence 157, App
C 35	129.6	5.2	15387	15	US-10-311-455-157	Sequence 1669, Ap
C 36	129.2	5.2	6668	15	US-10-311-455-1669	Sequence 16542, A
C 37	127	5.1	767	13	US-10-424-599-70401	Sequence 70401, A
C 38	125.8	5.1	712	13	US-10-424-599-109362	Sequence 109362,
C 39	125.2	5.0	508	17	US-10-021-323-4874	Sequence 4874, Ap
C 40	124.8	5.0	6145	15	US-10-311-455-945	Sequence 945, App
C 41	124	5.0	113515	15	US-10-311-455-2147	Sequence 2147, Ap
C 42	123.4	5.0	1533	13	US-10-282-122A-16542	Sequence 16542, A
C 43	123.2	5.0	529	17	US-10-021-323-10810	Sequence 10810, A
C 44	123	4.9	6171	15	US-10-311-455-761	Sequence 761, App
C 45	123	4.9	9539	15	US-10-239-676-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1

US-10-668-749A-1  
; Sequence 1, Application US/10668749A  
; Publication No. US20040110205A1  
; GENERAL INFORMATION:  
; APPLICANT: Agilent Technologies  
; TITLE OF INVENTION: Methods and Systems for Nanopore Data Analysis  
; FILE REFERENCE: 50112-1580  
; CURRENT APPLICATION NUMBER: US/10/668,749A  
; CURRENT FILING DATE: 2003-09-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1300  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-10-668-749A-1

Query Match	9.2%	Score 229.6;	DB 17;	Length 1300;
Best Local Similarity	48.6%	Pred No. 7,2e+23;		
Matches	625;	Conservative	0;	Mismatches 661; Indels 0; Gaps 0;
QY	1152	AAAGATGCACTGGTAAAAATCGAGACAAATATATAAAGGAAAGTTCAGGATTTTA	1211	
Db	1	AA	60	
QY	1212	GAAAGATTTTAGATCCAGTAAGGATATAATGTCTCAATGTCCTCAATGACAGATGAA	1271	
Db	61	AA	120	
QY	1272	TTGGCAAAAAATTTCAAGAGAGAAAGGTAAATAACGGGGAGAGAGAAATGATATAA	1331	
Db	121	AA	180	
QY	1332	GCTGCTCTTTTAGGAGAGATCAAAAGAGGTGAGAGAGAAATGACAGACTGTTAT	1391	



2896 AA 2837  
QY 1755 TATTTTACCGATGACACACAAAGCTATATATTAACATGGGAGATTAGAGATGAA 1814  
Db 2836 CGAAAAAAAAAAAAAAAAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2777  
QY 1815 GAAGGCGAAGGATTGGGAAAAATTAATTGAAGAAATTGAGTGATAGAGATGAGTTAAGA 1874  
Db 2776 AAAAAACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2717  
QY 1875 ACCAA-----ATTAAATAAGATATAAATAATTTATGCTCATGAAATGAGCTCTC 1929  
Db 2716 AAAAAAATCAAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2657  
QY 1930 TAAAGAAATGTAGATGTCAGCGAAATTTAAAGAGATTTAGAAAAAGTAAAAATCAGGAT 1989  
Db 2656 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2597  
QY 1990 TAGAAAAGTTAAAGATATCTTAAAGACAAATCTTAAATTTGAAGAAATTAAGGATACA 2049  
Db 2596 CAAAAACGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2537  
QY 2050 TC 2051  
Db 2536 AC 2535

RESULT 3  
US-10-437-963-77858/c  
; Sequence 77858, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 77858  
; LENGTH: 1204  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(1204)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_77718C.1  
US-10-437-963-77858

Query Match 6.7%; Score 167; DB 17; Length 1204;  
Best Local Similarity 51.9%; Pred. No. 3.9e-14;  
Matches 401; Conservative 0; Mismatches 366; Indels 5; Gaps 1;  
QY 1277 AAAAAATTTACAAAGAGAGAAAGGTAATAACGGGAGAGAAAGAAATGATAAGCTGT 1336  
Db 1185 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1126  
QY 1337 CTTTTTAGGAGAGATCAAAAGAGGATGAAGAGAAATGAGCAAGCTGTTAATTAGA 1396  
Db 1125 AATAAAGCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1066  
QY 1397 AGAAAAAATGCGAGAGAGATGAAGAGTGTGTTAATTTAGAGAGAGAAATTAGAGCT 1456  
Db 1065 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1006

QY 1457 TAAAAAGAGACTGAAGAGATGAAGATAAAGAAATAGAGAAAAAAGAAAAAAGAAAGT 1516  
Db 1005 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 946  
QY 1517 GAAAAAGCACAAGAAAGAAAAACACGACAAAGAGAAAAAGAAAAAAGAAAAAAGAAACA 1576  
Db 945 AAAAAAGACAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 886  
QY 1577 GCAGAGAAAGAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAA 1632  
Db 885 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 826  
QY 1633 -ACAAAAATTTAAAGAACTTGGGATATAAATAGATGAGATAAGTTGGAATNTTGTGTTAT 1691  
Db 825 TAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 766  
QY 1692 GAAAGTCAACCAAGTGTAAACCGAAGCAGTTATAGATAAATTTACGGGCTGTATAT 1751  
Db 765 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 706  
QY 1752 GATTATTTTACCGATGACAAACAAAAAGCTATATATATAAATGAGGAGATTTAGAAAGT 1811  
Db 705 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 646  
QY 1812 GAAGAGCGGAGGATTTGGGAAATTTATGAAAGAAATTTGAGTATAGATGAGTTA 1871  
Db 645 AAAAAATACTAAACATATATAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 586  
QY 1872 AGAACCAATTTAAATAAAGATAATAAAAAATTTATGCCATGAAAAATGAGCTCTCTA 1931  
Db 585 AAAAAATTAATGATAGATAAAGAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 526  
QY 1932 AAGAAAAATGATGATGTCAGCGAAATTTAAAGAGATTTAGAAAAAGTAAATCAGGATTA 1991  
Db 525 AAACCTAAAAAAGAAAAAGAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGTAA 466  
QY 1992 GAAAGGTTAAAGATATCTTAAAGACAAATTTCTAAATTTGAAGAAATTTAAAG 2043  
Db 465 AAAAAATAGAAAAAATTAATATCAATATATATTAATTAATTAATTAATTAATTAAT 414

RESULT 4  
US-10-221-714A-461/c  
; Sequence 461, Application US/10221714A  
; Publication No. US20040048254A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with  
; FILE REFERENCE: 5013.1005  
; CURRENT APPLICATION NUMBER: US/10/221,714A  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/02955  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: DE 10013847.0  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 540  
; SEQ ID NO 461  
; LENGTH: 6292  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

	Query Match	6.3%	Score 157;	DB 17;	Length 803;
	Best Local Similarity	51.8%;	Pred. No. 8.5e-13;		
	Matches 310;	Conservative 0;	Mismatches 288;	Indels 0;	Gaps 0;
Qy	1137	AAAGATGCAACTGGTAAAGATGCAACTGCTAAATATGCAGACAAAATATAAAGCGAAA	1196		
Db	798	AAUNGANAAAGAAANAAAAAAGAAAAAANAAAAAAGANAGAAAAA	739		
Qy	1197	GTTCAAGGATTTTGAAGAAAGATTTTAGATCCAGTAAAGGATAAAATGCTTCAAAATGTT	1256		
Db	738	AAAAAAGAAAGNAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAA	679		
Qy	1257	CCAAATAGCAGATCAATTGCGAAAAAAATTTACAAGAGAGAAAAAGCTTAATACGGGAA	1316		
Db	678	GAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA	619		
Qy	1317	GAGGAAAAATGATAAAGCTGCTTTTTAGGAGAGAAATCAAAAGAGGATCAAGAGAAAAAT	1376		
Db	618	AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAA	559		

1377	QY	GAGCAGACTGTTTAAATTTAGAGAAAAAATAATGCGGACAGAGATAGAAGTTGTGTTAATTA	1436
558	Db	AGAAAAAGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	499
1437	QY	GAAGAGAAAGAAATTTAGAAAGTTTAAAAAGAGACTCAAGAGATGAAGAGATAAAGAGAAATA	1496
498	Db	AAAAAATAAAAAAAAAAGAAAAAATAAAAAAAAAAAAAAAAAAAAAAGAAAAA	439
1497	QY	GAGAAACAAAAACAAGAAAGTGGAAAAAGCACAGAAAGAAAAACAACGACAGAGAAAG	1556
438	Db	AGAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA	379
1557	QY	AAACGAAAAAACAAGAACGACGAGAGAGAAAAAGAAAAACGAAAAACGAAAGAAACAAAGAAAA	1616
378	Db	AAAAAATAA	319
1617	QY	GAAGGAGACTTAAAAACAAATTTAAAAAACTTCGCGATAAATAGATAGATAAGTTGG	1676
318	Db	AAAGAAAAAATAA	259
1677	QY	AAATATTGATGGTATAGAAAGTCAAAACAGTGTAAAAACCGAAAGCAGTTATAGATAAAA	1734
258	Db	AAGAGAGAGAAAAAGAAAGAAAAAATAAAAAAAAAAAGAAAGANNAGNNNNNNNAGAGAAA	201

RESULT 6  
US-10-311-455-1931/c  
; Sequence 1931, Application US/10311455  
; Publication No. US20030143606A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Expression of Specific Genes

```

/ TITLE OF INVENTION: Diagnosis of diseases associated with the immune system by detecting
/ FILE REFERENCE: 5013.1014
/ CURRENT APPLICATION NUMBER: US/10/311.455
/ CURRENT FILING DATE: 2002-12-16
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537
/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 1931
/ LENGTH: 14006
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: 8289, 8310, 8313
/ OTHER INFORMATION: n is a or g o r t
US-10-311-455-1931

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	Query Match	6.2%	Score 154.2;	DB 15;	Length 14006;
	Best Local Similarity	53.6%;	Pred. No. 5.2e-12;		
	Matches 321;	Conservative 0;	Mismatches 278;	Indels 0;	Gaps 0;
Qy	1136	TAAAGATGCACACTGGTAAAGATGCAACTGGTAAAAATGCAGAACCAAAATATATAAAGGGAA			
Db	2500	TAAACAAATAAAAA			
Qy	1196	AGTTCAAGGATTTTGTAGAAAAAGATTTTGTAGTCCAGTAAGGATATAATTTGCTTCAAAATGG			
Db	2440	AAAAA			
Qy	1256	TCCAAATACAGATGAATTGGCAAAAAAATTTCAAGAGAGAGAAAGGTAATATAACGGGGA			
Db	2380	CCAAAATAAAAA			
Qy	2321	CAAAATAAAAA			
Db	2321	CAAAATAAAAA			

[illegible]

## RESULT 7

```

US-10-021-323-9336
; Sequence 9336, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCES: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 9336
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LTB3828-024-Q6-K6-C2
US-10-021-323-9336

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Query Match	6.2%	Score 154;	DB 17;	Length 627;
Best Local Similarity	52.9%;	Pred. No. 2.1e-12;		
Matches 331;	Conservative 0;	Mismatches 295;	Indels 0;	Gaps 0;
QY	1369	AAGAAAATGACGACGCTGTTAATTTAGAGAAAAAAATGCGAGAGGATAGAGAACTTG	1428	
Db	2	AAGGAAAAAA	61	
QY	1429	TTAATTTAGAGAGAAAAGATTAGAGCTTAAAAAAGAGACTGGAAGAGAGATGAAGATAAAG	1488	
Db	62	AGAAAAAATAAAAAAAAAAAGGAAAAAAAAAAAAAAAAAAGAAAAAAAAAAAA	121	
QY	1489	AAGAAATAGAGAAACAAAAACAGAGCTGGAAGAACGACAGAAAGGAAACACGACAAG	1548	
Db	122	AAAAAAAAAAGGAAAGAAAAAAGAAAAAATAAAAAAAAAAAAAAAAAAAGAAAAAA	181	
QY	1549	AAGAAAAAGAAACGAAAAAAAAAACAAGAACAGCAAGAGAAAAACGACAAGAC	1608	

Db 182 AAAAAAAAAAAAAAAAAAAAAAAAAAAGGAGAAAAAAAAAAAAAAAAAAAAAAAAA 241  
 Qy 1609 AAGAGAAAGAGAGAGCTTAAACCAAAATTAATAAATTCGCGATATAATAGATGAGA 1668  
 Db 242 AAGGAAAAAAAAAGAAA 301  
 Qy 1669 TAAGTTGGAATATTGATGGTATAGAAAGTCAACAGAGTGAACCGAAGCAGTTATAG 1728  
 Db 302 GAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 361  
 Qy 1729 ATAAATTTACGGGCTGTATATGATTATTTTACCGATGACACAAAGAGCTATATATA 1788  
 Db 362 AAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAA 421  
 Qy 1789 AATCATGGGAGATTTTGAAGAGTGAAGAGCGAGGATTTGGGAAATTTATTTGAAAGAT 1848  
 Db 422 AAAAAAAAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 481  
 Qy 1849 TGAGTGATCTAGAGTGTAGTAAAGTGAAGACCAATTAATAAGATATAATAAATATTATG 1908  
 Db 482 AAAAAAAAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 541  
 Qy 1909 CCCATGAAATGAGCTCTCTTAAAGAGAAATGTAGATGTACGCGAAATTTAAAGAGAT 1968  
 Db 542 AAAAAAAAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGAGA 601  
 Qy 1969 TAGAAGATTAATCTAGGATTTAGAA 1994  
 Db 602 AAGGAAAAAAAAAGAGAGAGAGAA 627

RESULT 8  
 US-10-312-841-2/c  
 ; Sequence 2, Application US/10312841  
 ; Publication No. US20030186277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Epigenomics AG  
 ; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC  
 ; FILE REFERENCE: E01/1208/WO  
 ; CURRENT APPLICATION NUMBER: US/10/312,841  
 ; CURRENT FILING DATE: 2002-12-30  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SEQ ID NO 2  
 ; LENGTH: 3673778  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 ; NAME/KEY: unsure  
 ; LOCATION: (379615)  
 US-10-312-841-2

Query Match  
 Best Local Similarity 6.1%; Score 152.8; DB 15; Length 3673778;  
 Matches 343; Conservative 0; Mismatches 317; Indels 0; Gaps 0;  
 Qy 1068 TTTGTGCTGATAAGTTCTTGCAAGATGTGCAACTGGTAAAGATGCAACTGGTAAAGAT 1127  
 Db 972186 TTTATTTTATTTTATTTTATTTTATCAATTAATAATAATACATACCCCTATATATCA 972127  
 Qy 1128 GCACTGGTAAAGATGCAACTGGTAAAGATGCACTGGTAAAGATGCAAGACAAATATA 1187  
 Db 972126 ACTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 972067  
 Qy 1188 AAAGGAAAGTTCAAGAGATTTTGAAGAAAGATTTTGAAGTCCAGTAAAGATTAATTCGT 1247  
 Db 972066 ACCACTACACTTCAACCTATCTAACCAAAATCTATCTCCAAAAAATAAATAAATAA 972007  
 Qy 1248 TCAATTTGGTCAATAGCAGATGATTTGGCAAAAAAATTTCAAGAGAGAGAAAGGTAAT 1307  
 Db 972006 AAAAAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 971947

Qy 1308 AACGGGGAAGAGAAATGATAAAGCTGCTCTTTTAGGAGAGAAATCAAAAGAGGATCAA 1367  
 Db 971946 AATATAA 971887  
 Qy 1368 GAAGAAATAGCAGCAGCTGTTAATTTAGAGAGAAATAATGCGGAGAGGATAGAGAGTT 1427  
 Db 971886 AA 971827  
 Qy 1428 GTTATTTAGAGAGAGAAATTTAGAAAGTTAAAAAGAGAGCTGAAGAGATGAAGATATA 1487  
 Db 971826 AA 971767  
 Qy 1488 GAAGAAATAGAGAAACAAAAACAAGAGAGTGAAGAAAGCAAGAGAAACCAACGACAA 1547  
 Db 971766 AA 971707  
 Qy 1548 GAAGAAAGAAACGAGAAACAAAAACAAGAGACAGCAAGAGAAAGAAACGACACAGAA 1607  
 Db 971706 AA 971647  
 Qy 1608 CAAGAGAAAGAGAGAGAGCTTAAACCAAAATTTAAAAAATTCGCGATAAAAATAGATGAG 1667  
 Db 971646 AA 971587  
 Qy 1668 ATAAGTTGCGATATTGATGTTATAGAAAGTCAACAGAGTGTAAACCGAAGCAGTTATA 1727  
 Db 971586 AA 971527

RESULT 9  
 US-10-221-714A-409/c  
 ; Sequence 409, Application US/10221714A  
 ; Publication No. US20040048254A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OLEK, Alexander  
 ; APPLICANT: PIEPENBROCK, Christian  
 ; APPLICANT: BERLIN, Kurt  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with  
 ; FILE REFERENCE: 5013.1005  
 ; CURRENT APPLICATION NUMBER: US/10/221,714A  
 ; CURRENT FILING DATE: 2003-01-21  
 ; PRIOR APPLICATION NUMBER: PCT/BF01/02955  
 ; PRIOR FILING DATE: 2001-03-15  
 ; PRIOR APPLICATION NUMBER: DE 10013847.0  
 ; PRIOR FILING DATE: 2000-03-15  
 ; PRIOR APPLICATION NUMBER: DE 10019058.8  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: DE 10019173.8  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: DE 10032529.7  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: DE 10043826.1  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 540  
 ; SEQ ID NO 409  
 ; LENGTH: 7442  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 ; NAME/KEY: unsure  
 ; LOCATION: 1792, 4861..4862  
 ; OTHER INFORMATION: n is a or g or c or t  
 US-10-221-714A-409

Query Match  
 Best Local Similarity 6.0%; Score 150.2; DB 13; Length 7442;  
 Matches 446; Conservative 0; Mismatches 468; Indels 5; Gaps 1;  
 Qy 1213 AAAAGATTTTAGATCCAGTAAAGGATATAAATTCCTTCAATGTCCTCAATAGCAGATCAAT 1272











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Db 31938 AAAAAAAAAACAAAAAACAACAAAAAACAACAAAAAACAACAAAAAACAACAAAAAACA 31879  
Qy 1936 AAAATGTAGATGTCAGCGAAATTAAGAAGATTTAGAAAAAGTAAAAATCAGGATTAGAA 1995  
Db 31878 AAAAAACAAAAAACAACAAAAAACAACAAAAAACAACAAAAAACAACAAAAAACAACATCC 31819  
Qy 1996 AGTTAAAGATATCTTAAGACAATCTAAATTTGAAGAAATTAAGGATACATC 2051  
Db 31818 CGCCGACCCCTACTAAAAATCCAAAAATTCGTAACAAATATATACACGAACATC 31763

Search completed: July 30, 2004, 05:21:06  
Job time : 2267 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: July 29, 2004, 16:02:38 ; Search time 6240 Seconds  
(without alignments)  
11901.802 Million cell updates/sec

Title: US-09-830-228-51  
Perfect score: 2487  
Sequence: 1 ATTATTATACGAAACCTT.....TTAAAGACACTTTGAAAGA 2487

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*\*
- 2: em\_esthum:\*\*
- 3: em\_estin:\*\*
- 4: em\_estmu:\*\*
- 5: em\_estov:\*\*
- 6: em\_estpl:\*\*
- 7: em\_estro:\*\*
- 8: em\_htc:\*\*
- 9: gb\_est1:\*\*
- 10: gb\_est2:\*\*
- 11: gb\_htc:\*\*
- 12: gb\_est3:\*\*
- 13: gb\_est4:\*\*
- 14: gb\_est5:\*\*
- 15: em\_estfun:\*\*
- 16: em\_estom:\*\*
- 17: em\_gss\_hum:\*\*
- 18: em\_gss\_inv:\*\*
- 19: em\_gss\_pln:\*\*
- 20: em\_gss\_vrt:\*\*
- 21: em\_gss\_fun:\*\*
- 22: em\_gss\_man:\*\*
- 23: em\_gss\_mus:\*\*
- 24: em\_gss\_pro:\*\*
- 25: em\_gss\_rod:\*\*
- 26: em\_gss\_phg:\*\*
- 27: em\_gss\_vri:\*\*
- 28: gb\_gss1:\*\*
- 29: gb\_gss2:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	234.8	9.4	1566	29	CG757757 P053-1-D0
C 2	232.8	9.4	1531	29	CG748014 P041-4-B0
C 3	226	9.1	1491	29	CG753221 P048-2-A0
C 4	223.4	9.0	1811	29	CG753732 P048-4-G0

RESULT 1  
CG757757/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

CG757757 1566 bp DNA linear GSS 24-OCT-2003  
P053-1-D07.zc Ppa EcoRI BAC Library Pristionchus pacificus genomic,  
genomic survey sequence.  
CG757757 GI:37986636  
GSS.  
Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 1566)  
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
Suntjer,J., van der Meulen,M. and Sommer,R.J.  
An integrated physical and genetic map of the nematode Pristionchus  
pacificus  
Mol. Genet. Genomics 269 (5), 715-722 (2003)  
22835951  
12884007  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071501371  
Fax: 00497071501498  
Email: raif.sommer@tuebingen.mpg.de

ALIGNMENTS

CC222065 CH261-11A  
CG751144 P045-3-E0  
CG747831 P041-3-B0  
CC23489 CH261-62N  
CG756607 P051-4-C0  
CG744327 P036-4-E0  
BE420745 HNM002-B0  
AL250012 Tetradon  
CC187638 CH261-98P  
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CG749971 P044-2-E0  
CG758143 P053-3-B1  
CG746828 P040-1-G1  
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CG744915 P037-3-F0  
CG754010 P049-2-C0  
CG74616 P039-2-A0  
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CC268594 CH261-67F  
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CG749578 P043-4-D1  
CG744200 P036-3-H0  
CG757211 P052-2-G0  
CG757918 P053-2-A0  
CF238805 AGENCOURT  
CG749445 P043-3-G0  
CC270526 CH261-119  
CG748584 P042-3-B0  
CG744840 P037-3-C0  
CG751608 P046-1-C1  
CG749744 P044-1-C1  
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Class: BAC ends.  
Location/Qualifiers  
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Best Local Similarity 42.6%; Pred. No. 8.9e-20;  
Matches 584; Conservative 0; Mismatches 786; Indels 0; Gaps 0;

QY 1107 AAAGATCGAAGTGAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGT 1166  
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QY 1167 AAAAAATCGACACAAAAATATAAAGGGAAGTTCAAGGATTTTTCAGAAAGATTTTTCAGAT 1226  
DB 1501 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1442

QY 1227 CCAAGTAAAGGATAAATGTCTTCAATGTCCATAGCAGATGAATGGCAAAAAAATTA 1286  
DB 1441 AA 1382

QY 1287 CAAGACGAAGAAGGTAAATACGGGAGAGAGAAATGATAAAGCTGCTTTTTCAGCA 1346  
DB 1381 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1322

QY 1347 GAAGAATCAAAAGAGGATGAAGAGAAATGACCAAGCTGTTAAATTTAGAGAGAAAAAAT 1406  
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QY 1407 GCGAGAGAGATGAAGAAGTTGTTAATTTAGAGAGAAAGATTAAGATTTTAAAAAGAG 1466  
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QY 1467 ACTCAAGAGATGAAGATAAGAGAAATAGAGAAAACAAAGCAAGCTGGAAGAAAGCA 1526  
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QY 1527 CAAGAAAGAAAACACGACAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1586  
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QY 1647 CTTGCGGATAAATAGATGAGATAGTGGAAATTTGATGATGATGATGATGATGATGAT 1706  
DB 1021 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 962

QY 1707 GTAAACCGAAGCAGTTATAGTAAATTCGGGCGCTGTATATGATTTTTCAGCAT 1766  
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QY 1767 GACAAACAAAAGCTATATATAAACAATGGGAGATTTTGAAGATCAAGAGCGCAAGGA 1826  
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QY 2007 TATCTTAAAGACAATTTCTAAATTTCAAGAAATTAAGAGATACATCAGTTACAGTCAGTAA 2066  
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QY 2067 TTATTTGGATGCTTTTTCAGTGAATCTAAATTTTTCAGTACACAAAAATACAGCTAGTAGA 2126  
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QY 2127 AAAGTTCACTGGCTGTTATTTTTCAGTGAATTTTCATTTGTTATGATATAGAAATGTTTTC 2186  
DB 541 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 482

QY 2187 TATCAAAACTTTTCAATTTTAAAGTGCAGAACTTATGCTGCTAAAGTGTGTTTATATAT 2246  
DB 481 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 422

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RESULT 2  
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DEFINITION P041-4-B02.2a Ppa EcoRI BAC Library Pristionchus pacificus genomic,  
genomic survey sequence.  
ACCESSION CG748014  
VERSION CG748014.1 GI:37968940  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
REFERENCE 1 (bases 1 to 1531)  
AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
Buntjer,J., van der Meulen,M. and Sommer,R.J.  
TITLE An integrated physical and genetic map of the nematode Pristionchus  
pacificus  
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)  
MEDLINE 22835951  
PUBMED 12884007  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends.  
Location/Qualifiers  
1..1531  
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1502 A 1502

CG753221/c

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LOCUS	P048-2-A01.za	BAC Library	Pristionchus pacificus genomic,	
DEFINITION	P048-2-A01.za	EcoRI		

genomic survey sequence.

ACCESSION CG753221  
VERSION CG753221.1  
KEYWORDS GI:37977480  
GSS.

ORGANISM

**AUTHORS** Srinivasan, J., Sin, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R. J.

**TITLE** An integrated physical and genetic map of the nematode *Pristionchus*

JOURNAL  
MEDLINE  
FUEMED  
Mol. Genet. Genomics 269 (5), 715-722 (2003)  
22835951  
12894007

Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany

Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends.

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/db xref=taxon:54126"
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Query: March					

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		Best Local Similarity	43.0%	Pred. NO. 1.1e-18;			
		Matches	580;	Conservative	0;	Mismatches	76;
						Indels	0;
						Gaps	0;

RESULT 3  
CG753221/c

LOCUS  
DEFINITION  
CG453221  
PpA EcoRI  
1491 bp  
linear  
DNA  
Prionionchus pacificus  
genomic,  
survey sequence.

CG753221  
ACCESSION  
CG753221.1  
VERSION  
GI:37977480  
KEYWORDS  
GSS.

SOURCE	ORGANISM
Pristionchus pacificus	
Pristionchus pacificus	

REFERENCE  
1 (bases 1 to 1491)  
Neodiplogasteridae; Pristionchus.  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasteriida;

**AUTHORS**  
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,  
Buntjer, J., van der Meulen, M. and Sommer, R. J.

**TITLE** An integrated physical and genetic map of the nematode *Pristionchus pacificus*  
**JOURNAL** Mol. Genet. Genomics 269 (5), 715-722 (2003)

MEDLINE 22835951  
PUBMED 12884007

COMMENT  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Contact: Sommer KJ

Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601362

Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .1491

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/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

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Matches 580;	Conservative	0;	Mismatches 769;	

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Db      1430 ANAAAAANNAANAAAAAANAAAAAANNNNNAANNAANAAAAAANAAAAAANNA 1371
Qy      1209 TTAGAAAGATTTTAGATCAGCTAAAGGATAAAATTCGTTCAATGGTCCATAGCAGAT 1268
Db      1370 ANAAAAAANAAAAAANAAAAAANNAANNAANAAAAAANAAAAAANNAAN 1311
Qy      1269 GAATTCGCAAAAAATTTACAGAGAGAAAGGTAATTAACGGGGAAGAGAAATGAT 1328
Db      1310 AAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANNAANNA 1251
Qy      1329 AAGCTGTCTTTTAGGAGAGAGATCAAAAGAGGATGAGAGAGAAATGAGCAGCTGTT 1388
Db      1250 AAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANNAANNA 1191
Qy      1389 AATTAGAGAAAAAATCGGAGAGAGATAAGAAAAAGTTGTTAATTTAGAGAGAGAGAA 1448
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Qy      1809 GATCAAGAGCGGAGGATTTGGGAAATTTATTCGAAAGATTTGAGTGATCTAGAGATGAG 1868
Db      770 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANNA 711
Qy      1869 TTAAGAACCAATTAATAAGATAATAAAAAATATTTATGCCATGAAATGAGCTCT 1928
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Qy      1929 CTAAAGAGAAATGTAGATGTCAGGAAATTTAAGAGAGATTTAGAAAAAGTAAATCAGGA 1988
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Qy      2109 AAAATAACAGCTAGTAGAAAAAGTTCACTGGCTGTTATTTTTTTGTAGATTTTCATTTGTTAT 2168
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Db      290 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANNA 231
Qy      2349 TTTAACTAGCCNAATACTCTTAAAGCAAAAAAGACAAATTTTACAGTCTCTTTGAAAGAAAT 2408
Db      230 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANNA 171
Qy      2409 CAAAAATACGTATATAAAACCGGAAAAA 2437
Db      170 AAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANNA 142

RESULT 4
CG753732/c
LOCUS   CG753732              1811 bp      DNA      linear      GSS 24-OCT-2003
DEFINITION   P048-4-G03.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,
              genomic survey sequence.
ACCESSION   CG753732
VERSION     CG753732.1  GI:37978509
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
            Pristionchus pacificus
            Neodiplogasteridae; Pristionchus.
REFERENCE   1 (bases 1 to 1811)
AUTHORS     Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
            Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE       An integrated physical and genetic map of the nematode Pristionchus
            pacificus
JOURNAL     Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE     22835951
PUBMED      12884007
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            Class: BAC ends.

FEATURES             Location/Qualifiers
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ORIGIN
Query Match      9.0%; Score 223.4; DB 29; Length 1811;
Best Local Similarity 41.2%; Pred. No. 2e-18;
Matches 542; Conservative 0; Mismatches 770; Indels 2; Gaps 1;

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Qy      1212 GAAAAATTTTAGATCCAGTAAAGGATAAAATTCGTTCAAATGCTCCATAGCAGATGAA 1271
Db      1620 NAAAAANNAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANAAAAAANNA 1561
Qy      1272 TTGCAAAAAAATTCAGAGAGAGAAAGGTAATTAACGGGGAAGAAATGATATA 1331
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1630 AA 1689  
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1690 TAGAAGTCAACCAAGTGTAAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1749  
1140 AA 1081  
1750 ATGATTATTTACCGATGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1809  
1080 AA 1021  
1810 ATGAG 1869  
1020 AA 961  
1870 TAAG 1929  
960 AA 901  
1930 TAAAG 1989  
900 AA 841  
1990 TAGAAG 2049  
840 AA 781  
2050 TCAGTTACAGTCAAGTATTTATTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2109  
780 AA 721  
2110 AATAACAGCTAGTAG 2169  
720 AA 661  
2170 AATATAG 2229  
660 AA 601  
2230 ATGTTGTTTATTTATATCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2289  
600 AA 541  
2290 GATGATATTTATATAG 2349  
540 AA 481  
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QY 2410 CAAAAATACGTAATATAAATACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2463  
Db 420 AA 367

RESULT 5  
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LOCUS CH261-11A13 RM1.1 CH261 Gallus gallus genomic clone CH261-11A13,  
DEFINITION genomic survey sequence.  
ACCESSION CC222065  
VERSION CC222065.1 GI:30546917  
KEYWORDS GSS.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 1716)  
AUTHORS Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,  
Warren, W., Graves, T., Mardis, E. and Wilson, R.  
Gallus gallus BAC End Reads  
Unpublished (2003)  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert Length: 182000 Std Error: 0.00  
Seq primer: RM1 TAGCACTCACTATAGGGAGA  
Class: BAC ends  
High quality sequence start: 905  
High quality sequence stop: 985.

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CH261 female Chicken library - for library and clone  
ordering information: http://www.chori.org/bacpac"

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Query Match 9.0%; Score 223.2; DB 28; Length 1716;  
Best Local Similarity 49.3%; Pred. No. 2.2e-18;  
Matches 637; Conservative 0; Mismatches 650; Indels 5; Gaps 2;

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Db 232 AA 291  
QY 1272 TTGGCAAAAAATTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1331  
Db 292 AA 351  
QY 1332 GCTGCTTTTATAG 1391  
Db 352 AA 411  
QY 1392 TTAG 1451  
Db 412 AA 471  
QY 1452 GAAGTTAAAAAG 1510







Db 1309 AAAAAAAAAAGAAAAAACAACAAAAAAGAAAAAAGAAAAAACAACAA 1368  
Qy 2277 GATTTCAGATTTTGATGATATTTATATAAGAAAAACAAAAAGAAATAGATAAATCTTAT 2336  
Db 1369 ACACAAAAAAGAAAAAAGAAAAAACAACAAAAACCAAAAAAAGAAAAAAGAAAAA 1428  
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RESULT 9  
CG756607/c 1298 bp DNA linear GSS 24-OCT-2003  
LOCUS P051-4-C04.yb Ppa EcoRI BAC Library Pristionchus pacificus genomic,  
DEFINITION genomic survey sequence.

ACCESSION CG756607  
VERSION CG756607.1 GI:37984341  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

REFERENCE 1 (bases 1 to 1298)  
Nediplogasteridae; Pristionchus.

AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,  
Buntjer,J., van der Meulen,M. and Sommer,R.J.  
TITLE An integrated physical and genetic map of the nematode Pristionchus  
pacificus

JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)  
MEDLINE 22835951  
PUBMED 12884007  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel.: 00497071601371  
Fax: 00497071601498  
Email: raif.sommer@uebingen.mpg.de  
Class: BAC ends.

FEATURES  
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Qy 1337 CTTTATTAGGAGAAAGAAATCAAAAGAGGATGAAGAGAAATGAGCAAGCTGTTAATTAGA 1396  
Db 1231 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1172  
Qy 1397 AGAAAAAATCGGAGAGAGATGAAGAGTTGTTAATTAGAGAGAAAGAAATGAGAACT 1456  
Db 1171 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1112  
Qy 1457 TAAAAAGAGACTGAAGAGATGAAGATAAAGAGAAATAGAGAAAAAAGAAACAAAGAACT 1516

Db 1111 NAANA 1052  
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Qy 1817 AGGCGAAGGATTTGGGAAAAATTTTGAAGAAATTTGAGTGATCTAGAGATGAGTTAAGAAC 1876  
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Db 451 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 392  
Qy 2177 AAATGTTTCTATCAAAACTTTTCAATTAAGAGTGCACAAACTATGCTAAAATGTTGT 2236  
Db 391 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 332  
Qy 2237 TTATTTATATATCTCTAGAGCTATGAGCTATACAAATGAGATTTTCAGATTTTGTATGATA 2296  
Db 331 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 272  
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Db 271 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 212  
Qy 2357 GCGNAAATTAATCTTAAAGCAAAAGACAAATNTTACAGTGTGTTGAAAGAAATGCAAAAT 2416  
Db 211 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 152  
Qy 2417 ACGTAATAAAACC 2430  
Db 151 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 138

RESULT 10  
CG744327/c  
LOCUS P036-4-E08.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CG744327



Email: herrmann@botanik.biologie.uni-muenchen.de  
International Triticaceae EST Cooperative (ITEC)  
<http://wheat.pw.usda.gov/genome>.

## FEATURES

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1. 1985
/organism="Hordeum vulgare subsp. vulgare"
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## ORIGIN

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Query Match 8.4%: Score 209.8: DB 29: Length 1036:

[illegible]

RESULT 12

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LOCUS

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 036N11 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL250012

VERSION AL250012.1 GI:7971024

KEYWORDS GSS; genome survey sequence.

SOURCE Tetraodon nigroviridis

ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.

REFERENCE 1

AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
Nat. Genet. 25 (2), 235-238 (2000)

TITLE

JOURNAL

MEDLINE 20296633

PUBMED 10835645

REFERENCE 2

AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
Genome Res. 10 (7), 939-949 (2000)

TITLE

JOURNAL

MEDLINE 20359837

PUBMED 10893143

REFERENCE 3 (bases 1 to 1036)

AUTHORS Genoscope.  
Direct Submission  
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)

TITLE

JOURNAL

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

SOURCE

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Location/Qualifiers  
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Db 426 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 485
QY 1632 AACAAATTTAAACAACTTGGGATAAATAGATGAGATGAGTTGGATATTTGATGTATA 1691
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QY 1692 GAAAGTCAAAACAAGTGTAAACCGAAAGCAGTTTATAGATAAATTTACGGGCGCTGTATAT 1751
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QY 1984 CAGATTAGAAAGGTTAAAGATATCTTTAAAGACAAATTCATAATTTGAAGAAATTAAG 2043
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LOCUS
DEFINITION P040-4-D10.2a Ppa EcoRI BAC Library Pristionchus pacificus genomic,
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genomic survey sequence.
CG747324 GI:37968250
VERSION CG747324.1
KEYWORDS Pristionchus pacificus
SOURCE Pristionchus pacificus
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 1211)
AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE An integrated physical and genetic map of the nematode Pristionchus
pacificus
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE 22835951
PUBMED 12884007
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 48.4%; Pred. No. 1.2e-16;
Matches 466; Conservative 0; Mismatches 496; Indels 1; Gaps 1;
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genomic survey sequence.
ACCESSION CG749971
VERSION CG749971.1 GI:37970948
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SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1377)
REFERENCE
AUTHORS Srinivasan,J., Sins,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE An integrated physical and genetic map of the nematode Pristionchus
pacificus
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE 22835951
PUBMED 12884007
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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Db 478 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 419
QY 1947 GTCAGCGAAATTAAGAGAGATTTAGAAAAAGTAAATCAGGATTAGAAAAAGTTTAAAGAA 2006
Db 418 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 359
QY 2007 TATCTTAAAGCAATTCATAATTTGAAGAAATTTAAGAGATACATCAGTTACAGTCA 2066
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Qy 2187 TATCAAAACTTTCAATTTAAAAAGTGCAAAACTATTGCTAAAAATGTTGTTTATTATAT 2246  
Db 178 NCACAAAACNVCANVTNAACTCAAAATATTTCAATAATTTTTCTTCTAACNCTAN 119  
Qy 2247 ACTCTCTAGAGCTATGACGTATACAAATGAGATTTTCAGATTTTTCAGATAAATTTATATAA 2306  
Db 118 TANANTNTTCACCAACCCCAAAAATAATAATATANCNCTTAATAATAAATAAATAAAN 59  
Qy 2307 GAAAAACAAAAA 2319  
Db 58 TANCNCTTAATA 46

Search completed: July 29, 2004, 20:55:42  
Job time : 6250 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2004, 16:08:39 ; Search time 179 Seconds  
(without alignments)  
7710.407 Million cell updates/sec

Title: US-09-830-228-51  
Perfect score: 2487  
Sequence: 1 ATTATTACACGAAACCTT.....TTAAGACACTTTGAAGA 2487

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	197.4	7.9	1498	1	US-08-118-469A-1
2	197.4	7.9	1498	1	US-08-309-119-1
3	144.4	5.8	7218	1	US-08-232-463-14
4	136	5.5	3095	6	5231168-1
5	127.4	5.1	4766	5	PCT-US93-07261-10
6	121.8	4.9	5361	3	US-08-973-462-2
7	121.8	4.9	6152	3	US-08-973-462-1
8	117.2	4.7	774	3	US-09-461-697-187
9	117.2	4.7	819	3	US-09-461-697-185
10	117.2	4.7	1669	3	US-09-461-697-184
11	116.6	4.7	696	3	US-09-461-697-193
12	116.6	4.7	699	3	US-09-461-697-191
13	116.6	4.7	717	3	US-09-461-697-189
14	110.2	4.4	1956	4	US-08-359-896B-1
15	110.2	4.4	1956	4	US-09-351-794A-1
16	107.8	4.3	5433	3	US-08-929-329-1
17	106.6	4.3	396	4	US-09-640-173-53
18	106.6	4.3	396	4	US-09-713-550-53
19	103.2	4.1	2223	1	US-08-257-073-4
20	102.6	4.1	19124	2	US-08-487-826B-13
21	100.6	4.0	1664976	4	US-08-916-421B-1
22	100	4.0	6866	4	US-10-204-708-20
23	98.8	4.0	3337	1	US-08-072-610-1
24	98.8	4.0	3337	2	US-08-719-822B-1
25	98.8	4.0	3337	3	US-09-092-458-1
26	96.6	3.9	240	1	US-08-628-417-6
27	95.4	3.8	2447	2	US-09-014-969-14

c	28	94.8	3.8	6306	4	US-10-204-708-50	Sequence 50, Appl
	29	92.6	3.7	3279	3	US-08-446-137B-1	Sequence 1, Appl
	30	90.8	3.7	1320	1	US-08-257-073-15	Sequence 15, Appl
	31	88.8	3.6	306	3	US-09-461-697-203	Sequence 203, App
c	32	88	3.5	929	4	US-09-671-317-14	Sequence 14, Appl
	33	88	3.5	1696	4	US-09-835-811-1	Sequence 1, Appl
c	34	87.6	3.5	1001	4	US-09-671-317-439	Sequence 439, App
	35	87	3.5	1298	3	US-08-948-705-3	Sequence 3, Appl
	36	87	3.5	1298	4	US-09-510-543-3	Sequence 3, Appl
c	37	86.2	3.5	10467	4	US-10-204-708-2	Sequence 2, Appl
	38	86	3.5	2394	4	US-09-800-729-33	Sequence 33, Appl
	39	85.4	3.4	1236	2	US-08-741-134-5	Sequence 5, Appl
c	40	85	3.4	1664976	4	US-08-916-421B-1	Sequence 1, Appl
c	41	84.8	3.4	5562	4	US-10-204-708-63	Sequence 63, Appl
	42	84.6	3.4	1276	3	US-09-177-325-2	Sequence 2, Appl
	43	84.6	3.4	1276	3	US-09-411-812A-2	Sequence 2, Appl
	44	84.6	3.4	1276	4	US-09-590-113-2	Sequence 2, Appl
	45	84	3.4	1891	3	US-08-973-462-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-08-118-469A-1  
; Sequence 1, Application US/08118469A  
; Patent No. 5656451  
; GENERAL INFORMATION:  
; APPLICANT: Flavell, Richard A.  
; APPLICANT: Fikrig, Erol  
; APPLICANT: Lam, Tuan T.  
; APPLICANT: Kantor, Fred S.  
; APPLICANT: Barthold, Stephen W.  
; TITLE OF INVENTION: NOVEL B. BURGDOFFER POLYPEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/118,469A  
; FILING DATE: 08-SEP-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/099,757  
; FILING DATE: 30-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: YU-102CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1498 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 129..644

FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 672..1364  
US-08-118-469A-1

Query Match 7.9%; Score 197.4; DB 1; Length 1498;  
Best Local Similarity 50.6%; Pred. No. 7.5e-26;  
Matches 564; Conservative 0; Mismatches 536; Indels 15; Gaps 3;

QY 901 GTTGATTAATAATATATTCGTTGTTTAAATGTAATGCTGAATGTAACACAAATATAT 960  
Db 1 GTTGTTAAATTAACATTTTCGTTTGTGTTAAATGTAACAGCTGGAATGTAACAAATAT 60

QY 961 ATATTTAAATCTTTGAAAAATTTGTAATTTGTTGGGTTGTTGTTAAATCTTTAAGCTTATGG 1020  
Db 61 ATATTTAAATCTTTGAAAAATTTGCAATTTATGTAATTTGTTGTTAAGATTAGCACTTATGG 120

QY 1021 AGTGGATTATGAATTAATAAATGAAATATTTATTTATTTGCTGTGTTATTTGCTGTGATTA 1080  
Db 121 AGTAACCTTATGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 180

QY 1081 GTTCTTCAAGATTGATGCACTGTTAAAGATGCAATCTGTAAGATGCAATCTGGTAAAG 1140  
Db 181 GTGCTTCAGATTCATCTTCTATATGATGAGCAAGTAGTGTGAGTCACAAAGTTAA 240

QY 1141 ATGCAACTGTTAAGATGCACTGTTAAATAATGCAAAATAAATAAATAAATAAATAAATAA 1200  
Db 241 AAATAGAATTTCTTAAATTTTACTGTAAAAATTTAAAAATAAAGATAAAGTGTAACTGGA 300

QY 1201 AAGGATTTTAAAGAAATTTTATAGATCCAGTAAAGATTAATTTGCTTCAATGTTCCAA 1260  
Db 301 CAGACTTAGAGATTTAGTTGTAAGAAAGAGAAATGTTATGATCGGTTTAAAGC 360

QY 1261 TAGCAGATGAATTTGGCAAAAAATTT---ACAAGAAGAGAAAAAGTAAATAACGGGGAAG 1317  
Db 361 CTGGGGACATTCGGCTACATCTTTCTTCAATTAAGAGGAAGTAGTTAATAACTTTGTA 420

QY 1318 AAGAAATGATTAAGTGTCTTTTGTAGGA-----GAAGATCAAAAGAGGATGAAG 1368  
Db 421 AGTAAATGATCTGAAGCGGATCAATTTAAACTAGTTTGTATTATGATTAAGGAAGAAC 480

QY 1369 AAGAAATGACGAAGCTGTTTAAATTTAGAAGAAAAAATCGGAAGAGGATAAGAAAGTTG 1428  
Db 481 AAAGTGTATAAATGTTATCCAAATTAAGAGATATAACAAAGATAGAAAAAATTTGATG 540

QY 1429 TTAATTTAGAGAAAGAAATTTAGAAGTTAAATAAGAGACTGAAGAGATGAAGATAAG 1488  
Db 541 GAACTGAATATATTACATTTTCAGGAGATAAAATTTAAGAAATTCAGGAGATAAGTTGCTG 600

QY 1489 AAGAAATAGAGAAACAAAAACAAAGAGTGGAAAAAGCACAAGAAAAACAAACACACAAAG 1548  
Db 601 AATATGCAATATCACTAGAGAGCTTAAGAGAAATTTAAATAGAAGTTGGAGTATAGG 660

QY 1549 AAGAAAGAAACGAAAAACAAAGAACAGCAAGAGAAAGAAACGAAACGACAGAAC 1608  
Db 661 AGAAGCTTATATGAATAAAAAAATGTTTATTTATTTTGTGCTATTTTTCGCTGATGTTT 720

QY 1609 AAAGAAAGAAAGAGAGCTTAAAAACAAATTTAAAAAATCTGCGGATAAAATAGATGAGA 1668  
Db 721 CTTGCAAGAAATTAACAATGACAAAGATTTAGAAGGTCAGTGCNAGATTTAGAAAGTT 780

QY 1669 TAAGTTGGAATATTTGATGATGAAGAGTCAACAGAGTAAACCGAAAGCAGTTATAG 1728  
Db 781 CAGAACAAAAATGCAAAAAACAAAGACAGAGATAAAAAACAAAGTTGAAGGATTTTATAG 840

QY 1729 ATAAATTTAGCGGCTGTATATGNTATTTTACCGATGACACAAAAAAGCTATATATA 1788  
Db 841 AAATCTTAGAGACAAAGATTTGAATACATTTGATACAAAGATATAAAGAGATTGAAA 900

QY 1789 AAACATGGGAGATTTTAGAGATGAAGAGGCGAAGGATTTGGAAAAATTTTGAAGAAT 1848  
Db 901 AACAAATTCAGAATTAAGGACACAAATAAATAAATTTAGAGGCTAAAAAACTTCTCTTA 960

QY 1849 TGAGTGATCTAGAGATCAGTTAAGAACCAAAATTAATAAAGATAATAAAAAATATTATG 1308  
Db 961 AAACATATTTCTGAGTATGAAGACAAATATAAAAAATTAAGAAAAATTTAAAGATAA-- 1018

QY 1909 CCCATGAATGAGCCTCCTCTCTAAAGAAATGTAGATGTCAGCGAAATTTAAAGAGATT 1968  
Db 1019 -GAAGAACTTTGAAGATAAAATTAAGGAAGCTTGAAGAGAGCTTTAAAAAAGAAAAAGAGG 1077

QY 1969 TAGAAAAAGTAAATCAGGATTAGAAAAAGGTTAAA 2003  
Db 1078 AGAGAAAAAAGCTTTAGAGATGCTTAAGAGAAA 1112

RESULT 2  
US-08-909-119-1  
; Sequence 1, Application US/08909119  
; Patent No. 5807685  
; GENERAL INFORMATION:  
; APPLICANT: Flavell, Richard A.  
; APPLICANT: Fikrig, Erol  
; APPLICANT: Lam, Tuan T.  
; APPLICANT: Kantor, Fred S.  
; APPLICANT: Barthold, Stephen W.  
; TITLE OF INVENTION: NOVEL B. BURGDOFFER POLYPEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/909,119  
; FILING DATE: 11-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/118,469  
; FILING DATE: 08-SEP-1993  
; APPLICATION NUMBER: US 08/099,757  
; FILING DATE: 30-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: YU-102CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9090  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1498 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 129..644  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 672..1364  
US-08-909-119-1

Query Match 7.9%; Score 197.4; DB 1; Length 1498;  
Best Local Similarity 50.6%; Pred. No. 7.5e-26;  
Matches 564; Conservative 0; Mismatches 536; Indels 15; Gaps 3;

QY	901	GTTCATTAAATTTATATTTGCGTTTTGTTTAATATGTAATAGCTGAATGTAACAAAAATTAT	960
DB	1	GTTCGTTAAAAATTACATTTGCGTTTTGTTTAATATGTAACAGCTCAATGTACAAAAATTAT	60
QY	961	ATATTTAAATCTTTGAAAAATTGTAAATTTGTTGGGGTTGTGTAACACTTAAGCGCTTATGG	1020
DB	61	ATATTTAAATCTTTGAAAAATTGCAATTAATATGTAATTTGTTGGTAAGNATAGGACTTATGG	120
QY	1021	AGTCGATATGAATTAATAAATAATGAAATATATTTATTTGCTGCTGTAATTTGCTGCTGATAA	1080
DB	121	AGTAACTTATGAATAAAGAAAAATGTTTATTTGTTTATGCTGTGTTTTTATACTTTATAG	180
QY	1081	GTTCTTGCAGATTGATGCAACTGGTAAAGATGCAACTGCTTAAAGATGCAACTGTGTAAG	1140
DB	181	GTGCTTGCAGATTTCATCTTCATATGATGAGCAAGTAGTGGTGAGTCAAAGTTTAAAA	240
QY	1141	ATGCAACTGTGTAAGATGCAACTGGTAAAAATGCAGAACAAAAATATAAAAAGGGAAGTTTC	1200
DB	241	AAATAGAAATTCCTTAAATTTTACTGTAAAAATTTAAAAATAAAGATATAAAGTGTAACTGG	300
QY	1201	AAGGATTTTTTAGAAAAGATTTTAGATCCAGTAAAGGATAAAATGCTTCAATGTTGCTCAA	1260
DB	301	CAGACTTAGGAGATTTAGTTGTAGAAAAGAAAGAAATGGTATTTGATACCGGTTTAAACG	360
QY	1261	TAGCAGATGAATTCGCCAAAAAAATTT---ACAAGAAAGAAAGAAAGGTAAATAACCGGGAAG	1317
DB	361	CTGGGGACATTCGGCTACATCTCTTTCAATTAGAAGAGGAAGTAGTTTAAATACTTTGTAA	420
QY	1318	AAAGAAATGATAAGCTGTCTTTTAGA-----GAAGATCAAAGAGGATGAAG	1368
DB	421	AAGTAATGACTGAAGGGCGGATCATTTAAACTAGTTTGTATTTATGGAATAAAGGAAGAC	480
QY	1369	AAGAAAAATGACCAAGCTGTTAAATTTAGAAGAAAAAAATGCGGAGAGGATAAGAAAGTTG	1428
DB	481	AAAGTGTTTATAAATGGTATCCAAAAATAAAGAGATAATAACAAAGATAGAAAAAATTCGATG	540
QY	1429	TTAATTTAGAGAGAAAGAAATTAGAAGTTTAAAAAGAGACTGAAGAGATGAAGATAAG	1488
DB	541	GAACCTGAATATATTACATTTTCAGAGATATAAATTAAGAAATTCAGGAGATAAAGTTGCTG	600
QY	1489	AAGAAATAGAGAAAACAAAAACAGAAAGTGAAAAAGCACAAGAAAGAAAAACAACGACAAG	1548
DB	601	AATATGCAATATCACTAGACAGCTTAAGAAGATTTTAAAAATAGAAGTTGGAAGTATAGG	660
QY	1549	AAGAAAGAAACGAAAAAAAACAGAACAGCAGAAAGAAAGAAACGAAAAACGACAAGAAC	1608
DB	661	AGAAAGCTTATGAATTAATAAAAAATGTTTATTTTGTGCTATTTTTCGCTGATAGTTT	720
QY	1609	AAAGAAAGAAAGCAGAGCTAAAAACAAAAATTTAAAAAACTTGGCGATAAAATAGATGAGA	1668
DB	721	CTTGCAAGAAATTATACAACTAGCAAGATTTTAGAAGGTCAGTGCAGATTTAGAAATTT	780
QY	1669	TAAGTTGGAATATTGATGGTATAGAAAGTCAACCAAGTGTAAACCAGAAAGCAGTTATAG	1728
DB	781	CAGAACAAAAATGCAAAAAAAAACAGAACAGAGATAAAAAAACCAAGTTTGAAGGATTTTTT	840
QY	1729	ATAAAATTCGCGGCGCTGTATATGATTTTATCCGATGACACAAAAAGCTATATATA	1788
DB	841	AAATTCAGAGACAAAGATTTGAAATACATTTGATACAAAGATATATAAGAGATTTGAAA	900
QY	1789	AAACATGGGGAGATTTAGAGATGAAGAGCGGAAGGATTTGGGAAAAATTTATGGAAGAAAT	1848
DB	901	AACAAATTCAGAAATTAAGGACACAAATAAATAAATTAGAGGCTTAAAAAAACCTTCTCTTA	960
QY	1849	TGAGTGATCTAGAGATGAGTTAAGAACCAAAATTTAAATAAGATAATAAAAAATATTATG	1908
DB	961	AAACATATCTGAGTATGAGAACCAATATAAAAAATTAAGAAAAATTAAGATAA---1018	
QY	1909	CCCATGAAAAATGAGCTCCTCTTAAAGAAAAATGTAGATGTACGGAAATTTAAAGAGATT	1968
DB	1019	-GAAAGAACTTGAAGATAAAATTAAGGAACTTTGAAGAGAGCTTAAAAAGAAAAAGAGG	1077

QY 1969 TAGAAAAAGTAAATCAGGATTAGAAAAAGGTTAAA 2003  
 DB 1078 AGAGAAAAAAGCTTTTAGAAGATGCTTAAGAGAAA 1112  
 RESULT 3  
 US-08-232-463-14/c  
 ; Sequence 14, Application US/08232463  
 ; Patent No. 5670367  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DORNER, F.  
 ; APPLICANT: SCHEIFLINGER, F.  
 ; APPLICANT: FALKNER, F. G.  
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 1800 Diagonal Road, Suite 500  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22313-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/232,463  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/935,313  
 ; FILING DATE:  
 ; APPLICATION NUMBER: EP 91 114 300.6  
 ; FILING DATE: 26-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)836-9300  
 ; TELEFAX: (703)683-4109  
 ; TELEX: 899149  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7218 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; CLONE: pTZgpt-Fis  
 US-08-232-463-14

[illegible]









Db 5002 TGAAGAGTTAAAGCGAAGAAAGAAAAATAGAAAAAAGTTGAAGAAAGTGTAGTGG 5061  
Qy 1922 GCTCCTCTAAAGAAAAATCTAGATGTCAGCGAAATTAAGAGAGATTTAGAAAAAGTAA 1981  
Db 5062 TCTTAAAAACACGTAGACGAGTAATGAATATGTTCAAAAAATGATAAAGAGTTGA 5121  
Qy 1982 ATCAGGATTAGAAAAAGTTAAAGATATCTTAAGACAAATCTTAA--TTTGAAGAAAT 2038  
Db 5122 TAAAGAGTATCTAAAGCTTTAGAAATCAAAAAATGATGTTACTAATGTTTAAACAAA 5181  
Qy 2039 TAAAGGATACATCAGTTCAGTCACTAGTAAATATATATTGGATGCTTTAGATGTAACHTAAT 2098  
Db 5182 TCAAGATTTTTTTAGTAAAGTTAAACCTTCGTAAGAAATATAAAGTATTTGCTGCACC 5241  
Qy 2099 TTACGTACACAAAATTAACAGCTAGTAGAAAAAGTTCACTGGCTGTATTTTTTTGTAGATT 2158  
Db 5242 ATTCATATCGCGTTGCAGCAATTCATCATATGATGTTGGTCTCTTACATTTCTTT 5301  
Qy 2159 TCATTGTTATGATATAGAAATGTTTCTATCAAACTTTTCATTTAAAAAGTGCAAAAC 2218  
Db 5302 ATTTTCATCATGTTGTAACAATAGCTTCTTCACTTACTTATTATCAAAAAGTTGACAAAAC 5361  
Qy 2219 TATTGCTTAAAAATGTTGTTTATTATATATCTCTAGAGCTATGAGTATACAAATGAGA 2278  
Db 5362 TATAATTAATAAAGAGAGACCGTTTATTCACTTTGATTTGATCTTTAAGNAATTT 5421  
Qy 2279 TTTTCAGATTGTTGATGATAATTTATATAAGAAAAACAAAAAGAAATAGATAAACTTATA 2338  
Db 5422 AAAACATATTATTAACAACAATGAAGAAAAATTTAGTAAGAAAAAATAAATGTAAT 5481  
Qy 2339 ACAAGCTCTATTTAACTAGCCNATTAACCTTAAGCAAAAAAGACAAATNTACGTGCTG 2398  
Db 5482 AGAAGTAAACAACAAGCTGAGAAAAAAGGTAATGTAAGGTTAAACAATAAACCAGAA 5541  
Qy 2399 TTGAAGAATGCAAAAAATACGTAAATAAAACCGGAAAAA 2437  
Db 5542 AACAACTAAAGTTGATAAAAAATAAAGTACCGAAAAA 5580

## RESULT 8

US-09-461-697-187  
; Sequence 187, Application US/09461697  
; Patent No. 6277974

## GENERAL INFORMATION:

; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.

; APPLICANT: Barney, Shawn

; APPLICANT: Thomas, Mary Beth

; APPLICANT: Portbury, Stuart D.

; APPLICANT: Puranam, Kasturi

; APPLICANT: Katz, Lawrence C.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

; FILE REFERENCE: 10001-005-999

; CURRENT APPLICATION NUMBER: US/09/461,697

; CURRENT FILING DATE: 1999-12-14

; NUMBER OF SEQ ID NOS: 466

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 187

; LENGTH: 774

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-461-697-187

Query Match 4.7%; Score 117.2; DB 3; Length 774;

Best Local Similarity 50.3%; Pred. No. 4.9e-12;

Matches 324; Conservative 0; Mismatches 308; Indels 12; Gaps 1;

Qy 1035 AAAAAATGAAAAATATTATTATTGCTGCTGATTTGCTGCTGATAGTTCTTGAAGATT 1094

Db 55 ABAATGACACAAAAAGTATATGATGGAAGAAAAACATAGATACAGTCCCAAGCAATT 114

Qy 1095 GATCAACTGCTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAA 1154  
Db 115 GCTGAACCAAGCAAGAGCAAGTGTGTTGAAGAGACTACATGAAATGCTTAAAAATGGA 174  
Qy 1155 GATCAACTGCTAAAGATGCAAGCAAAATATATAAAGGGAAGTTCAGGAGTTTTCAGAA 1214  
Db 175 GAAGCCAAATTCACAGAGGCCACAGCTTCTGAAAAAGAAATTTGTGGAAGTAAAAAGAA 234  
Qy 1215 AAGATTTTATGATCCAGTAAAGGATAAAATTCCTTTCAATGCTCCAAATAGCAG-- 1266  
Db 235 AATATTGAGATGCCACGAAAGGGAGGAGAAAGAAAGAGCAGTGGCAGCAGAGTA 294  
Qy 1267 ----ATGAATTTGGCAAAAAAATTACAAGAAAGAAAGGTAAATAACGGGAAAGAA 1322  
Db 295 AAAAATGAAGAAAGATGCAAAAAGAGATGAAGAAGATCAAAAACGAAGAGAAAGGGA 354  
Qy 1323 AATGATAAGCTGCTCTTTTATAGGAGAGAGATCAAAAGAGGATGAAGAGAAATGACCA 1382  
Db 355 GCTGAAAAGAGACAAAAGATGAAAAGGGGGAAGAGATGAAAAGAGGATAAAAATGGA 414  
Qy 1383 GCTGTTAATTTAGAGAAAAAATCGGAGAGAGATGAAGAAAGTGTTAATTTAGAAGAG 1442  
Db 415 AATGAGAAAGGAGAGATGCAAAAAGAGAGATGGAATAAAGGTGAAGACGGA 474  
Qy 1443 AAGAATTTAGAACTTAAAAAGAGACTGAAGAGATGAAGTAAAGAGAAATAGAGAA 1502  
Db 475 GGAATGAGAGATGGAAGAAAGAGAGAGATGAAAAGAGAGAGAGAGAGAGAGAGAG 534  
Qy 1503 CAAAAACAAGAAAGTGGAAAAAGCACAAGAAAGAAACAAACGACAAAGAAAGAAAGCA 1562  
Db 535 GAACAGAGTTGGAAGAGAGATGAAGTGGAAAAAGAGAGAGAGAGATAAAAAGAGGG 594  
Qy 1563 AAAAAACAAGAACAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAG 1622  
Db 595 AAGATGCTAAAGTCAAAAGAGATGAAAAAGAGAGAGAGATGAAAAAGAGAGATGAAG 654  
Qy 1623 AGAGCTAAAAACAAAATTTAAAAAATTCGCGATATAAATAGATGA 1666  
Db 655 GGAATGAGGAAGAGCTGGAAGAAAGAGAGAGATTTAAAGA 698

## RESULT 9

US-09-461-697-185  
; Sequence 185, Application US/09461697  
; Patent No. 6277974

## GENERAL INFORMATION:

; APPLICANT: COGENT NEUROSCIENCE, Inc.

; APPLICANT: Lo, Donald C.

; APPLICANT: Barney, Shawn

; APPLICANT: Thomas, Mary Beth

; APPLICANT: Portbury, Stuart D.

; APPLICANT: Puranam, Kasturi

; APPLICANT: Katz, Lawrence C.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

; FILE REFERENCE: 10001-005-999

; CURRENT APPLICATION NUMBER: US/09/461,697

; CURRENT FILING DATE: 1999-12-14

; NUMBER OF SEQ ID NOS: 466

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 185

; LENGTH: 819

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-461-697-185

Query Match 4.7%; Score 117.2; DB 3; Length 819;

Best Local Similarity 50.3%; Pred. No. 5e-12;

Matches 324; Conservative 0; Mismatches 308; Indels 12; Gaps 1;

Qy 1035 AAAAAATGAAAAATATTATTATTGCTGCTGATTTGCTGCTGATAGTTCTTGAAGATT 1094

Db 100 A A A A T G A A G C A A A A A G T G A T A T G A T G G A A G A A A A C A T A G A T C A A G T C C C C A C A G A T T 159  
 Qy 1095 G A T G C A A C T G T T A A G A G T C A A C T G T T A A G A G T C A A C T G T T A A G A G T C A A C T G T T A A 1154  
 Db 160 G C T G A A A C C A A G C A A G A G C A G T T G T T G A A G A G A C T A C A A T C A A A A T G C T A A A A T G G A 219  
 Qy 1155 G A T G C A A C T G T T A A A A T C A G A A C A A A A T A T A A A A G G A A A G T T C A A G A T T T T A G A A 1214  
 Db 220 G A A G C C A A A A T T A C A G A G G C A C A G T T C T G A A A A A A A A T T G T G A A G A T A A A A G A A G A A 279  
 Qy 1215 A A G A T T T T A G A T C C A G T A A A A G G A T A A A A T T G C T T C A A A T G G T C C A A T A G C A G - - - - - 1266  
 Db 280 A A T A T T C A A G A T C C A G A A A A G G A G G A G A A A G A A A G A A G A C A G T G C A C A G A A G T A 339  
 Qy 1267 - - - - - A T G A A T T G C A A A A A A A T T A C A A G A A G A A A A A G T A A A T A A C C G G G A A G A A G A A 1322  
 Db 340 A A A A A T G A A G A A G A G A T C A G A A A G A A G A T G A A A A G A T C A A A A C C G A A G A A A A G G G A A 399  
 Qy 1323 A A T G A T A A A G C T G T C T T T T T A G A G A A G A A T C A A A A G A G A T C A A A A A A A A A A T C A G C A A 1382  
 Db 400 C T T G A A A A G A A C A A A A G A T G A A A A G G G A A G A A G A T G A A A G A G A T A A A A T G C A 459  
 Qy 1383 G C T G T T A A T T A G A A A A A A A A A T G C G A A G A G A T A A G A A A G T T G T T A A T T T A G A A G A G 1442  
 Db 460 A A T G A A A A G A G A G A T G C A A A A G A G A A A G A A G A T G G A A A A A A A A A A G G T G A A G A C G A A A 519  
 Qy 1443 A A A G A A T T A G A A C T T A A A A A G A G A C T G A A G A G A T G A A A A A A A A A A A A A A A A T A G A A A 1502  
 Db 520 G G A A A T G G A G A G A T G A A A A A G A A A A G A A G A G A T G A A A A G A G A A A G A A G A C A G A A A 579  
 Qy 1503 C A A A A A C A A A A G T G G A A A A G C A C A 1562  
 Db 580 G A A A C A G A G T T G G A A A A G A G A T G A A T G G A 639  
 Qy 1563 A A A A A C A A A C A G C A G A G A A A A A A A A A C G A A A A C G A C A G A C A G A C A A A A A A A A A A A A G G 1622  
 Db 640 A A A G A T G T A A A G T C A A A A A A A A A T G A 699  
 Qy 1623 A G A G C T A A A A A C A A A A T T A A A A A A C T T G C G A T A A A A A T A G A T G A 1666  
 Db 700 G G A A A T C A G A A G A G A G T G G A A A A G A A A G A A G A A G A T T T A A A G A 743

RESULT 10  
 US-09-461-697-184  
 ; Sequence 184, Application US/09461697  
 ; Patent No. 6277974  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.  
 ; APPLICANT: Lo, Donald C.  
 ; APPLICANT: Barney, Shawn  
 ; APPLICANT: Thomas, Mary Beth  
 ; APPLICANT: Portbury, Stuart D.  
 ; APPLICANT: Purnam, Kasturi  
 ; APPLICANT: Katz, Lawrence C.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
 ; FILE OF INVENTION: CELL DEATH  
 ; FILE REFERENCE: 10001-005-999  
 ; CURRENT APPLICATION NUMBER: US/09/461,697  
 ; CURRENT FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 466  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 184  
 ; LENGTH: 1669  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-461-697-184

Query Match 4.7%; Score 117.2; DB 3; Length 1669;  
 Best Local Similarity 50.3%; Pred. No. 5.6e-12; Indels 12; Gaps 1;  
 Matches 324; Conservative 0; Mismatches 308;

Qy 1035 A A A A A A T G A A A A T A T T A T T A T T T G C T G T A T T T T G C T G T A A G T T C T T C A A G A T T 1094  
 Db 179 A A A A T G A A G C A A A A A A G T A T A T G A T G A A A A A A A C A T A G A T C A A G T C C C A A G A G T T 238  
 Qy 1095 G A T C A A C T G T T A A A G A T C A A C T G T T A A A G A T C A A C T G T T A A A G A T C A A C T G T T A A 1154  
 Db 239 G C T G A A A C C A A G A A G C A G T T G T T G A A G A A G A C T A C A A T G A A A A T G C T A A A A T G G A 298  
 Qy 1155 G A T C A A C T G T T A A A A T C A G A A C A A A A T A T A A A A G G A A A G T T C A A G A T T T T A G A A 1214  
 Db 299 G A A C C A A A A T T A C A G A G G C A C C A G T T C T G A A A A A A A A A T T G T G A A G T A A A A A G A A 358  
 Qy 1215 A A G A T T T T A G A T C C A G T A A A A G G A T A A A A T T G C T T C A A A T G G T C C A A T A G C A G - - - - - 1266  
 Db 359 A A T A T T C A A G A T C C C A G A A A A A G G G A G A A A A A G A A A G A A G A C A G T G C A G C A G A A G T A 418  
 Qy 1267 - - - - - A T G A A T T G C A A A A A A A T T A C A A A A G A 1322  
 Db 419 A A A A A T G A A A G A A G A T C A 478  
 Qy 1323 A A T G A T A A A G C T G T C T T T T T A G A G A A A A A T C A A A A G A G A T C A A A A A A A A A A A A A A A A 1382  
 Db 479 G C T G A A A A G A A G A A A A G A T G A A A A A G G G A A A G A G A T G A A A A A A A A A A A A A A A A A 538  
 Qy 1383 G C T G T T A A T T A G A A A A A A A A A T G C G A A G A G A T A 1442  
 Db 539 A A T G A A A A G A A G A G A T G C A 598  
 Qy 1443 A A A A A T T A G A A C T T A 1502  
 Db 599 G G A A A T G G A A A G A T G G A 658  
 Qy 1503 C A A A A A C A A A A G T G G A A A A A A A A A C A 1562  
 Db 659 G A A A C A G A G T T G G A A A A G A A A T G A A T G G A 718  
 Qy 1563 A A A A A C A A A C A G C A G A G A 1622  
 Db 719 A A A G A T G T A A A G T C A A A A A A A A A T G A 778  
 Qy 1623 A G A G C T A A A A A C A A A A T T A A A A A A C T T G C G A T A A A A A T A G A T G A 1666  
 Db 779 G G A A A T C A G A A G A G A G T G G A A A A G A A A A G A A A G A T T T A A A G A 822

RESULT 11  
 US-09-461-697-193  
 ; Sequence 193, Application US/09461697  
 ; Patent No. 6277974  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.  
 ; APPLICANT: Lo, Donald C.  
 ; APPLICANT: Barney, Shawn  
 ; APPLICANT: Thomas, Mary Beth  
 ; APPLICANT: Portbury, Stuart D.  
 ; APPLICANT: Purnam, Kasturi  
 ; APPLICANT: Katz, Lawrence C.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
 ; FILE OF INVENTION: CELL DEATH  
 ; FILE REFERENCE: 10001-005-999  
 ; CURRENT APPLICATION NUMBER: US/09/461,697  
 ; CURRENT FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 466  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 193  
 ; LENGTH: 696  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-461-697-193

Query Match 4.7%; Score 116.6; DB 3; Length 696;  
 Best Local Similarity 51.3%; Pred. No. 6.1e-12;

	Matches	297; Conservative	0; Mismatches	279; Indels	3; Gaps	1;
Qy	1088	CAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAAC	1147			
Db	45	CAAGCAAGAAGCAGTCTGTGAAGAAGACTACAATGAAATGCTAAAAATCGAGAGGCCAA	104			
Qy	1148	TGTTAAAGATGCAACTGGTAAAAATGCAGAAACAAATATATAAAGGGGAAAGTTTCAAGGATT	1207			
Db	105	AATTACAGAGGCCACCAGCT---TCTGAAAAAGAAATTTGTGGAATGTAAGAAGAAATAT	161			
Qy	1208	TTTAGAAAAAGATTTTAGATCCAGTAAAGGATAAAAATTTGCTTCAAAATGGTCCCAATAGCAG	1267			
Db	162	TGAAGATGCCACAGAAAAGGGAGGAGAAAAGAAAGAACAGTGGCAGCAGAAAGTAAAAAA	221			
Qy	1268	TGAATTCGCAAAAAAATTTACAAGAAAGAAAAAGGTAAAAATACGGGGAAGAGAAAAATGA	1327			
Db	222	TGAAGAAGAAGATCAGAAAGAAGATGAAGAAGATCAAACCGAAGAGAAACGGGAAGCTGG	281			
Qy	1328	TAAAGCTGTCTTTTAGGAGAAGNATCAAAGAGGATGAAGAGAAAAATCAGCAAGCTGT	1387			
Db	282	AAAAGAAGAACAAGATGAAAAGAGGGGAAGAGATGGAAAAAGAGATAAAAAATCGAAATGA	341			
Qy	1388	TAAATTTAGAAGAAAAAATCGGAAGAGGATTAAGAAATGTTTAAATTTAGAAGAGAAAG	1447			
Db	342	GAAAGGAGAGATGCCAAGAAGAAAGAGATGAAAAAAGAGGTGAGACGGAAAAAGGAAA	401			
Qy	1448	ATTAGAAGTTAAAAAGAGACTGAAGAAGATGAAGATAAAGAGAAATAGAGAAACAAA	1507			
Db	402	TGAGAGAAGATCGAAAAAGAGAAAGCAGAAGATGAAAAAGAGGAAAGACAGAGAAAGAAC	461			
Qy	1508	ACAAGAGTGGAAAAACCAAGAAAGAAAACACGACAGAGAGAAAGAAACGAAAAAA	1567			
Db	462	AGGAGTTGGAAAGAGAGNATGAGATGGAAAGAGAGAGGGGAGATATAAAAAAGAGGGGAAAG	521			
Qy	1568	ACAAGAACCAAGAGAAAAAGAAAACGAAACCGACAGAGAACAAAGAAAAAGAGAGAGC	1627			
Db	522	TGTAAGAGTCAAAGAAGATGAAAGAAGAGAGAGAAGATGGAAGAGAGATGAAGCTGGAAA	581			
Qy	1628	TAAAAACAAAAATTAAAAAAATCTCCGGATTAATAATAGATGA	1666			
Db	582	TGAGGAGAGAGCTGGAAAAAGAGAGAAAGAAAGATTTAAAGA	620			

RESULT 12  
US-09-461-697-191  
; Sequence 191, Application US/09461697  
; Patent No. 6277974  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Purnam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; TITLE OF INVENTION: CELL DEATH  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/461,697  
; CURRENT FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 191  
; LENGTH: 699  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-461-697-191

Query Match 4.7%; Score 116.6; DB 3; Length 699;  
Best Local Similarity 51.3%; Pred. No. 6.1e-12;  
Matches 297; Conservative 0; Mismatches 279; Indels 3; Gaps 1;

QY	1088	CAAGATTGATGCACCTGGTAAAGATCAACTGGTAAAGATGCAACTGGTAAAGATGCAAC	1147
Db	48	CMACCAAGAAGCAGTTGTTTGAAGAAGACTACAATGAAAATGCTAAAAATGGAGAAGCCAA	107
QY	1148	TGGTAAAGATGCCAAGCTGGTAAAAATGCAGAACCAAATAATAAAGGGAAGAACTTCAAGGATT	1207
Db	108	AATTACAGAGCGCACCGACT--TCTGAAAAGAAGAAATGTGGNAAGTAAAGAGAGAAATAT	164
QY	1208	TTTAGAAAAAGATTTTAGATCCAGCTAAAGGATAAAAATTCCTCAAATGGTCCAATAGCAGA	1267
Db	165	TGAAGATGCCACAGAAAAGGGAGGAGNAAAGNAAAGACAGTGGCAGCAGAACTAAAAA	224
QY	1268	TGAATTTGGCAAAAAAATTACAAGAGAGAAAAAGGTAAATAACGGGGAAGAGAAAAATGA	1327
Db	225	TGAAGAAGAAGATCAGAAAAGAAAGATGAAGAAGATCAAAACGAAGAGAAATGGGGAAGCTGG	284
QY	1328	TAAAGCTGTCTTTTAGGAGAAGAANTCAAAGAGGATGAGAGAGAAATGAGCAAGCTGT	1387
Db	285	AAAAGAAGACAAAGATGAAAAAGGGGAAGAGATGGAAGAAGGATTAANAATCGAAATGA	344
QY	1388	TAATTTAGAGAAGAAAAAATCGGAAGAGGATAGAAAAGTTGTTTAAATTTAGAAGAGAAAAGA	1447
Db	345	GAAAGGAGAGATGCCAAAAGAGAAAGACNAGTGC AAAA AAGGTCAAGACCGGAAAAGGAAA	404
QY	1448	ATTAGAAGTTAAAAAGAGACTGAAGAGAGATGAAGATAAAGAAAGAAATAGAGAAAACAAA	1507
Db	405	TGGAGAGAGATCGAAAAAGAGAAAGAGAGAAGATGAAAAAGAGGAAGAGACAGAAAAGAAAC	464
QY	1508	ACAGAAGTGGA AAAAGCCACAGAAAGAAACCAACGACAGAGAGAAAGAAACGAAAAA	1567
Db	465	AGGATTTGGAAAAGAGAGATGAAGATGGAAAAGAGAGAGGGAGATATAAAAAGAGGGGAAAAGA	524
QY	1568	ACAAGACACAGAAAGAAAAGAAAACGAAACGACAGAAACCAAGAAAAGAAAAGGAGAGC	1627
Db	525	TGTA AAAGTCAAGAAGATGAAAAGACAGAGAGAAGATGGAAAAGAGAGATCAACGTGGA	584
QY	1628	TAAAAACAAAATTA AAAA ACTCCGGATAAAATAGATGA	1666
Db	585	TGAGGAGAGAGCTCGAAAAGAGAAAAGAGAGATTTTAAAAGA	623

RESULT 13

```

RES001 13
US-09-461-697-189
; Sequence 189, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-189

```

Query Match 4.7%; Score 116.6; DB 3; Length 717;  
Best Local Similarity 51.3%; Pred. No. 6.2e-12;

QY 1088 CAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAAC 1147

Db 66 CAAGCAAGAGCAGTGTTCGAGAGAGCTACAAATGAAATGCTAAATAATGGAGAGCCAA 125  
Qy 1148 TGGTAAGATGCACTGTTAAATATCGAGAACAAATATATAAGGGAAGTTCAAGATT 1207  
Db 126 AATTACAGAGCCACAGCT--TCTGAAAGAAATTTGTGGAAGTAAAGAGAAATAT 182  
Qy 1208 TTTAGAAAGATTTAGATCCAGTAAAGGATAAAATTTGCTTCAATGGTCCCAATAGCAG 1267  
Db 183 TGAAGATCCACAGAAAGGAGAGAAAGAAAGAGCAGTGGCAGCAGAGTAAATAA 242  
Qy 1268 TGAATTCGCAAAAAATTAACAAGAGAGAAAGGTAATTAACCGGGAAGAGAAATGA 1327  
Db 243 TGAAGAAAGAGATCAGAAAGAGATGAAGAGATCAAAACGAGAGAGAAAGGGAAGCTGG 302  
Qy 1328 TAAAGCTGTCTTTTAGGAGAGAAATCAAAAGAGAGATGAAGAGAGAAATGAGCAAGCTGT 1387  
Db 303 AAAGAAGACAAAGATGAAGAGGGAAGAGATGGAAGATGGAAGAGAGATGAAGATGA 362  
Qy 1388 TAATTTAGAGAAAAATCGGAGAGAGATGAAGAGATTTGTTTAATTTTGAAGAGAAAGA 1447  
Db 363 GAAAGGAGAGATGCAAAAGAGAGAAAGAGATGCAAAAGAGGTTGAAGACGGAAGGAAA 422  
Qy 1448 ATTAGAGTTTAAAGAGAGCTGAAGAGATGAAGATGAAGAGAGAAATAGAGAGAAAGA 1507  
Db 423 TGGAGAGATGGAAAGAGAGAGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482  
Qy 1508 ACAAGAGTGGAAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1567  
Db 483 AGGAGTTGGAAGAGAGATGAAGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542  
Qy 1568 ACAAGAGCAG 1627  
Db 543 TGTAAAGTCAAGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 602  
Qy 1628 TAAAGCAAAATTAATAAACTTCGGATTAATAATAGATGA 1666  
Db 603 TGAGAGAGAGCTGGAAAG 641

## RESULT 14

US-08-559-896B-1  
; Sequence 1, Application US/08559896B  
; Patent No. 6310046  
; GENERAL INFORMATION:  
; APPLICANT: Patrick E. Duffy  
; APPLICANT: Christian F. Ockenhouse  
; TITLE OF INVENTION: SEQUESTIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John Moran  
; STREET: USA MEMC MCMR-JA  
; CITY: FORT DETRICK, FREDERICK  
; STATE: MARYLAND  
; COUNTRY: USA  
; ZIP: 21702-5012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.5  
; SOFTWARE: Microsoft Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/559, 896B  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Moran, John  
; REGISTRATION NUMBER: 26,313  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 619-2065

; TELEFAX: (301) 619-7714  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1956 base pairs  
; TYPE: Nucleic acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; US-08-559-896B-1

Query March 4.4%; Score 110.2; DB 4; Length 1956;  
Best Local Similarity 45.1%; Pred. No. 9.4e-11; Indels 30; Gaps 5;  
Matches 633; Conservative 0; Mismatches 740;

Qy 1079 AAGTTCTTTCGAAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAA 1138  
Db 528 AATTATAGTATGTATAGAGAGATATAAGTAAACAAAATATAAAGACCTTAATTAATAA 587  
Qy 1139 AGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAA 1198  
Db 588 TGAAGAGAAACAAATTAAGGATAAAAAACAAAAGAGATATAGATATAACCAAAAGAA 647  
Qy 1199 TCAAGGATTTTTAGAAAAGATTTTAGATCCAGTAAAGGATAAAAATTCCTTCAATGTGTC 1258  
Db 648 AAAAAAGATATAGATATAGATGTAGACATAGATATAAGATATACATAAAGATCATGTAGA 707  
Qy 1259 AATAGCAGATGAATTCGCAAAAAATTTACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1318  
Db 708 AGAATTATACGAGAGATTAATAAACAACCTTAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 767  
Qy 1319 AGAAATGATAAAGCTGTCTTTTAGGAGAGAGATCAAAAGAGAGATCAAAAGAGAGATCA 1378  
Db 768 AGACGCAATATATAGATATACCTTAGAGAGATTTAGATAGATGAACAGAGACGATTTATA 827  
Qy 1379 GCAAGCTGTTAATTTAGAAG 1438  
Db 828 TAGAGTATACCTAGAGAGATTTAGAAAAATAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 887  
Qy 1439 AGAGAGAGATTTAGAGTTTAAAGAGAGAGCTGGAAGAGAGATGAAGATGAAGAGAGAGAG 1498  
Db 888 AGAAAAATTTACAAAAATTTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 947  
Qy 1499 GAAACAAAAACAAGAGTGGAAAAAGCACAAGAAAAAGAAAAACAAGCACAAGAGAGAGAGAG 1558  
Db 948 TAAAAATATATGAGAGAGATTTAAACAAAAATGAGTAGTGAATTCACATGTAGAGAGAG 1607  
Qy 1559 ACGAAAAAACAAGACAGCAG 1618  
Db 1008 AGCAATATTACAGATATACAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1667  
Qy 1619 AAGGAGAGCTAAAAACAAAAATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1678  
Db 1068 TAGACTTTTATAAGAGAGATTT-----AGATAGAGATGATAGAGAGAGAGAGAGAG 1115  
Qy 1679 TATTGATGGTATAGAAAGTCAAAAGTGTAAACCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1738  
Db 1116 TGAATTCCTCCATGAGAAATTTAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1175  
Qy 1739 GGGGCTGTATATGATTTTTCCTGATGACACAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1798  
Db 1176 TAAAAATGAATCTAACAAAAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1234  
Qy 1799 AGATTTAGAGATGAAG 1858  
Db 1235 ACAATATGATGATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1289  
Qy 1859 TAGAGATGAGTTTAAAG 1918  
Db 1290 AATTAATAGCAG 1349  
Qy 1919 TGAGCCTCTCTAAAG 1978  
Db 1350 AAATTTAGACAG 1409

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QY 1979 AAAATCAGGATTAGAAAAAGGTTAAAGAAATATCTTAAAGACAATTCT-----AAAT 2028
Db 1410 AATTAAAGAGACAAAAGTTAAATGTTTCCATATAGTGAATTTTAAATTCAAAAGT 1469
QY 2029 TTGAAGAAATTAAAGGATACATCAGTTTACAGTCAGTAAATATATTTGGATGCTTTTAGATG 2088
Db 1470 AGGAAAGATATACACACCAATTCACATTAAGAGGAAATCAAGTAGATGTTGTCAGGAA 1529
QY 2089 TAACTAAATTTTACGTACACAAATTAACAGCTAGTAGAAAAAGTTCACTGCTGTTATTTT 2148
Db 1530 AATATTTTCAGATTATTCAGAGGATATATATAAAATTAAGGCCAAAGGATTAACACTGA 1589
QY 2149 TTTGTAGATTTCATTTGTTATGAATATAGAAATGTTTCTATCAAACTTTTCATTTTAAAAA 2208
Db 1590 AATGTTTAGAT--AATAATAGGAAATTAACAAATTTGATATATAAAATGTTGATGATATA 1647
QY 2209 GTCCAAAAACTATGCTTAAAAAGTTGTTTATTTATATCTCTCTAGAGCTATGAGTAT 2268
Db 1648 AAAAAATGTTGGAGATATAAAAAGTGTGGAGATATAAAAAGTGTGATGATATAACAAT 1707
QY 2269 ACAATTCAGATTTCAGATTTTGTATGATAATTTATATAAGAAAAACAAAAAGAAATAGAT 2328
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Db 1888 GCGGAGAAAAAACCAAACTTTGA 1910

RESULT 15
US-09-351-794A-1
; Sequence 1, Application US/09351794A
; Patent No. 6641815
; GENERAL INFORMATION:
; APPLICANT: DUFFY, PATRICK E.
; APPLICANT: OCKENHOUSE, CHRISTIAN F.
; TITLE OF INVENTION: SEQUESTIN
; FILE REFERENCE: 38644-175519
; CURRENT APPLICATION NUMBER: US/09/351,794A
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: 08/559,896
; PRIOR FILING DATE: 1995-11-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 1956
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-351-794A-1

Query Match 4.4%; Score 110.2; DB 4; Length 1956;
Best Local Similarity 45.1%; Pred. No. 9.4e-11;
Matches 633; Conservative 0; Mismatches 740; Indels 30; Gaps 5;

QY 1079 AAGTTCCTGCAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAA 1138
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Db 1290 AATAATTAAGCACACAAATAATAATTAATGAAAAATGTAAGTTGAATTTAGTTGTCAG 1349
QY 1919 TGAGCTCTCTAAAGAAATGATAGTGTAGCGAAATTAAGAGAAATTTAGAAAAAGT 1978
Db 1350 AATTTAGACAAAGGATAAAGGAGCCAGATAGAGATATATAGACTATTTTAAACAAAGA 1409
QY 1979 AAAATCAGGATTAGAAAAAGGTTAAAGAAATATCTTAAAGACAATTCCT-----AAAT 2028
Db 1410 AATTAAAAAGACAAAAATGTTAATGTTTCCATATAGTGAATTTTAAATTCAAAAGT 1469
QY 2029 TTGAAGAAATTAAGGATACATCAGTTACAGTCACTAGTAAATTTATTTGGATGCTTTTAGATG 2088
Db 1470 AGGAAAGATAACACACCAATTCACATAAGAGGAAATCAAGTAGATGTTGTCAGGAA 1529
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Db 1590 AATGTTTAGAT--AATAATAGGAAATAACAAATTTGATATAAATAAATGTTGATGATATA 1647
QY 2209 GTGCAAAACTATTCCTAAAAATGTTGTTTATTTATATACCTCTAGAGCTATGAGTAT 2268
Db 1648 AAAAAATGTTGGAGATATAAAAAGTGTGGAGATATAAAAAGTGTGATGATATAAACAAT 1707
QY 2269 ACAATTCAGATTTCAGATTTTGTATGATAATTTTATAAAGAAAAACAAAAAGAAATAGAT 2328
Db 1708 GTTGATGGTATAAATAAAGTGTGATATAAATAAATGTTGATGATATAAATAAATCTTGTAT 1767
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Qy	2389	TACAGTGTCTGTGAAGAATGC	AAAAATACGTAATAAAAAACCGGAAAAAGTGTCTTTTA	2448
Db	1828	AACAATGTGGCGGATATAA	CAATCTCTGTAGATATATACACCGTTGACATATAGACGAA	1887
Qy	2449	GAATCGGAAAAAGAAATTTG	TAA	2471
Db	1888	GCGGAGAAAAAACCAATCT	TGA	1910

Search completed: July 30, 2004, 02:04:10  
Job time : 190 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: July 29, 2004, 14:59:18 ; Search time 960 seconds  
(without alignments)  
11005.488 Million cell updates/sec  
Title: US-09-830-228-51  
Perfect score: 2487  
Sequence: 1 ATTATTACAGAACCTTGAAGA 2487  
Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3373863 seqs, 2124099041 residues  
Total number of hits satisfying chosen parameters: 6747726  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : N\_Geneseqn\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

ALIGNMENTS  
RESULT 1  
AAX20298  
ID AAX20298 standard; DNA; 2487 BP.  
XX AC AAX20298;  
XX DT 04-MAY-1999 (first entry)  
XX DE Borrelia burgdorferi polynucleotide sequence #51.  
XX KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
XX KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
XX KW infection; diagnosis; characterisation; detection; ds.  
XX OS Borrelia burgdorferi.  
XX PN W095858943-A1.  
XX PD 30-DEC-1999.  
XX PF 18-JUN-1999; 98WO-US012764.  
XX PR 20-JUN-1997; 97US-0050359P.  
XX PR 22-JUL-1997; 97US-0053344P.  
XX PR 22-JUL-1997; 97US-0053377P.  
XX PR 03-SEP-1997; 97US-0057483P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PA (MEDI-) MEDIMMUNE INC.  
XX PI Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
XX PI Smith HO;  
XX WPI; 1999-081217/07.  
XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
XX products for the detection, diagnosis, characterisation, prevention and  
XX therapy of infections, particularly Lyme disease.  
XX Claim 1; Page 1028-1029; 1128pp; English.  
XX AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
XX Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
XX detection, diagnosis, characterisation, prevention and therapy of Bb  
XX infections, e.g. Lyme disease. They can also be used for the production  
XX of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2485	99.9	2487	2 AAX20298	Aax20298 Borrelia
2	1083	43.5	1083	2 AAX61815	Aax61815 B. burgdo
3	979	39.4	979	2 AAX61816	Aax61816 B. burgdo
4	917.2	36.9	35515	2 AAX20252	Aax20252 Borrelia
5	827.4	33.3	2892	2 AAX20292	Aax20292 Borrelia
6	784	31.5	3129	2 AAX20285	Aax20285 Borrelia
7	733.8	31.5	5805	2 AAX20268	Aax20268 Borrelia
8	658.2	26.5	3653	2 AAX20280	Aax20280 Borrelia
9	493	19.8	2532	2 AAX20295	Aax20295 Borrelia
10	415.4	16.7	521	2 AAX20398	Aax20398 Borrelia
11	394.6	15.9	1047	2 AAX61805	Aax61805 B. burgdo
12	389	15.6	979	2 AAX61806	Aax61806 B. burgdo
13	385.4	15.5	1039	2 AAX61812	Aax61812 B. burgdo
14	385.4	15.5	1125	2 AAX61811	Aax61811 B. burgdo
15	336.8	13.5	9542	2 AAX20260	Aax20260 Borrelia
16	229.2	9.2	780	2 AAT10840	Aat10840 B. burgdo
17	197.4	7.9	1498	2 AAX83837	Aax83837 B. burgdo
18	188.8	7.6	1686	2 AAX87587	Aax87587 DNA encod
19	185.8	7.5	3399	2 AAT05868	Aat05868 Chicken l
20	175.6	7.1	6668	6 ABL33697	Ab133697 Human imm
21	173.6	7.0	6644	2 AAX33181	Aax33181 Base sequ
22	173.6	7.0	7372	2 AAX33182	Aax33182 Base sequ
23	173.6	7.0	7797	2 AAX33180	Aax33180 Cowpox vi

CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
XX  
SQ Sequence 2487 BP; 1021 A; 241 C; 453 G; 770 T; 0 U; 2 Other;

Query Match 99.9%; Score 2485; DB 2; Length 2487;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TAATGCTAAATTTGGTCTCTTTAAACCTATGTTTGGATTTTTCAGAAAAATAGTACGTC 120  
Db 61 TAATGCTAAATTTGGTCTCTTTAAACCTATGTTTGGATTTTTCAGAAAAATAGTACGTC 120

Qy 121 TTGATCAAGATTTTCTCATTAAATGATTTTGTGCTGCTTTGGATAGCCTCGAAT 180  
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Qy 181 CTTCGTAGTGTAAACAAATTTCTTAATACAGTTACATTTCTTTTGGCCACATTTA 240  
Db 181 CTTCGTAGTGTAAACAAATTTCTTAATACAGTTACATTTCTTTTGGCCACATTTA 240

Qy 241 CTTTATGTTGTATAAGTTTTCATTTTGCCTTAAAGTTGAAATATCTTGCATTT 300  
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Db 301 TTACTTTTTCAGTTGCGTCCCTGCGAGCACTTATTCGGAGTAATGTAAACCAAC 360

Qy 361 CAGATTTTGCATCAGCTTGTTTAAGAGTTTGTATGATTTTCAATTTAGTTTGCATTT 420  
Db 361 CAGATTTTGCATCAGCTTGTTTAAGAGTTTGTATGATTTTCAATTTAGTTTGCATTT 420

Qy 421 TTGGGTCAAATAAATTTAGGAGTTGGCTTTGAAGCTTTTTPAGTGGCTTAGAGAA 480  
Db 421 TTGGGTCAAATAAATTTAGGAGTTGGCTTTGAAGCTTTTTPAGTGGCTTAGAGAA 480

Qy 481 TTTTGTAGTAAATTTTAAAGAAATTTCTTTTCAATTTATAGTTTGTATGATCTTGTATA 540  
Db 481 TTTTGTAGTAAATTTTAAAGAAATTTCTTTTCAATTTATAGTTTGTATGATCTTGTATA 540

Qy 541 ATTTAAGCATAAATCTATGTTGAAATTTTAAATTAAGATAATTTATTCATGTCATAA 600  
Db 541 ATTTAAGCATAAATCTATGTTGAAATTTTAAATTAAGATAATTTATTCATGTCATAA 600

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Qy 661 ATGTAATTTATATTTTACCAAAACCAAAATTTAGTCAATTTGTGCTCTTCATTTG 720  
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Db 841 GTATGTTTGTAGTCTTTTAAATGAGAGGCAATTTGCAATGAGAGATTTTATAGGGA 900

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Db 961 ATATTAAATCTTTGAAAAATTTGTAATTTGTTGGGTTGTTGTTAAACTTAAGGCTTATGG 1020

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Db 1081 GTTCTTGCAGATTTGATGCACTCGTAAAGATGCAACTGTTAAAGATGCAACTGTTAAAG 1140

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Qy 1201 AAGGATTTTAAAGATTTTATAGTCCAGTAAAGATTAAGATTTGCTTCAATTTGTTCCAA 1260  
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Qy 1381 AAGCTGTTAATTTAG 1440  
Db 1381 AAGCTGTTAATTTAG 1440

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Db 1441 AGAAGAGATTTAG 1500

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Db 1501 AACAAAAACAG 1560

Qy 1561 GAAAAAACAG 1620  
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Db 1741 GGCCTGTATATGATTTATTTTACCGATGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1800

Qy 1801 ATTTAGAGAGATTAAG 1860  
Db 1801 ATTTAGAGAGATTAAG 1860

Qy 1861 GAGATGAGTTAAG 1920  
Db 1861 GAGATGAGTTAAG 1920

Qy 1921 AGCCTCTCTAAAG 1980  
Db 1921 AGCCTCTCTAAAG 1980

Qy 1981 AATCAGGATTTAG 2040  
Db 1981 AATCAGGATTTAG 2040

QY 2041 AAGATACATCAGTTACAGTCAGTAATATATATGATGCTTTAGATGTAACATAATTTT 2100  
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QY 2041 AAGGATACATCAGTTACAGTCAGTAATATATATGATGCTTTAGATGTAACATAATTTT 2100  
DB |||||  
QY 2101 ACGTACACAAATACAGTCAGTAAGAAAGTTCACTGGCTGTTATTTTGTAGATTTC 2160  
DB |||||  
QY 2101 ACGTACACAAATACAGTCAGTAAGAAAGTTCACTGGCTGTTATTTTGTAGATTTC 2160  
DB |||||  
QY 2161 ATTCTTATGATATAGAAATGTTTCTATCAAACTTTTCAATTTAAAAAGTGCATAAATA 2220  
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QY 2461 GAATTTGTTAAAGACACTTTGAAAAGA 2487  
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QY 2461 GAATTTGTTAAAGACACTTTGAAAAGA 2487  
DB |||||

## RESULT 2

AAAX61815  
ID AAX61815 standard; DNA; 1083 BP.  
XX  
AC AAX61815;  
XX  
DT 19-JUL-1999 (first entry)  
XX  
DE B. burgdorferi antigenic protein coding sequence, f51-2.nt.  
XX  
KW Antigenic protein; vaccine; Lyme disease; infection; detection; ss.  
XX  
OS Borrelia burgdorferi.  
XX  
PN WO9859071-A1.  
XX  
PD 30-DEC-1998.  
XX  
PF 18-JUN-1998; 98WO-US012718.  
XX  
PR 20-JUN-1997; 97US-0050359P.  
PR 22-JUL-1997; 97US-0053344P.  
PR 22-JUL-1997; 97US-0053377P.  
PR 03-SEP-1997; 97US-0057483P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PA (MEDI-) MEDIMUNE INC.  
XX  
PI Choi GH, Erwin AL, Hanson MS, Lathigra R;  
XX  
PI WPI; 1999-199980/16.  
DR  
DR P-PSDB; AAY20118.  
XX  
PT New isolated Borrelia burgdorferi nucleic acids - used to develop  
PT products for the diagnosis, prevention and treatment of diseases caused  
PT by Borrelia, particularly Lyme disease.  
XX  
XX Claim 1; Page 203-204; 275pp; English.  
PS  
XX This sequence encodes a Borrelia burgdorferi (Bb) protein of the

CC invention, which is suitable for use in a vaccine. The Bb polypeptides  
CC can be used in vaccines for eliciting protective antibodies to members of  
CC the Borrelia genus, particularly for the use against Lyme disease in  
CC humans and animals. They can be used for preventing or attenuating an  
CC infection caused by a member of the Borrelia genus. The products can also  
CC be used for detection of members of the Borrelia genus  
XX

SQ Sequence 1083 BP; 523 A; 91 C; 235 G; 234 T; 0 U; 0 Other;

Query Match 43.5%; Score 1083; DB 2; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 5.3e-136;  
Matches 1083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1044 AAAATATTTATTTATTTGCTGTATTTGCTGTATTAAGTCTTTCGCAAGATTGATCAACT 1103  
DB |||||  
QY 61 AAAATATTTATTTATTTGCTGTATTTGCTGTATTAAGTCTTTCGCAAGATTGATCAACT 120  
DB |||||  
QY 1104 GGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACT 1163  
DB |||||  
QY 121 GGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACT 180  
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QY 1164 GGTAAAAATGCAAGAACAAAATATATAACGGAAAGTTCAGGATTTTGAAGAGATTTTA 1223  
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QY 1284 TTACAAGAGAGAAAGTAAATAACCGGGAAGAAAGAAATGATAAGCTGTCTTTTAA 1343  
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QY 301 TTACAAGAGAGAAAGTAAATAACCGGGAAGAAAGAAATGATAAGCTGTCTTTTAA 360  
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QY 1344 GGAGAGAGATCAAAAGAGAGTGAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 1403  
DB |||||  
QY 361 GGAGAGAGATCAAAAGAGAGTGAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 420  
DB |||||  
QY 1404 AATCGGAGAGAGTGAAGAGAGTGAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 1463  
DB |||||  
QY 421 AATCGGAGAGAGTGAAGAGAGTGAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 480  
DB |||||  
QY 1464 GAGACTGAAGAGATGAAGATAAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 1523  
DB |||||  
QY 481 GAGACTGAAGAGATGAAGATAAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 540  
DB |||||  
QY 1524 GCACAAGAGAGAGTGAAGATAAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 1583  
DB |||||  
QY 541 GCACAAGAGAGAGTGAAGATAAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 600  
DB |||||  
QY 1584 GAAAAGAGAGAGTGAAGATAAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 1643  
DB |||||  
QY 601 GAAAAGAGAGAGTGAAGATAAAGAGAAATGAGCAAGCTGTTAATTTAGAGAGAAAA 660  
DB |||||  
QY 1644 AACTTCGGATTAATAGATGAGATAAGTGGATATTTGATGATAGAGAGTCAACA 1703  
DB |||||  
QY 661 AACTTCGGATTAATAGATGAGATAAGTGGATATTTGATGATAGAGAGTCAACA 720  
DB |||||  
QY 1704 AGTGTAAACCGAAGCAGTTATAGATAAATTTACGGGCTGTATATGATTTTATACC 1763  
DB |||||  
QY 721 AGTGTAAACCGAAGCAGTTATAGATAAATTTACGGGCTGTATATGATTTTATACC 780  
DB |||||  
QY 1764 GATGACACAAAAAGCTATATATAAATCATGGGAGATTTAGAGATGAAGAGGCGAA 1823  
DB |||||  
QY 781 GATGACACAAAAAGCTATATATAAATCATGGGAGATTTAGAGATGAAGAGGCGAA 840  
DB |||||  
QY 1824 GCATTGGCAAAATTTATTGAAAGAGATTCAGTGATCTAGAGATGAGTTAAGACCAATTA 1883  
DB |||||  
QY 841 GCATTGGCAAAATTTATTGAAAGAGATTCAGTGATCTAGAGATGAGTTAAGACCAATTA 900  
DB |||||

1894	AATAAGAGTAATAAAAAATATATATGCCCATGAAAATGAGCCTCCTCTTAAGAGAAAATGTGA	1943
QY		
901	AATAAGATATAAAAAAATATATATGCCCATGAAAATGAGCCTCCTCTTAAGAGAAAATGTGA	960
DB		
1944	GATGTCGCGGAAATTAAGAGAGATTTTAGAAAAAGTAAATCAGGATTAGAAAAGGTTAAA	2003
QY		
961	GATGTCGCGGAAATTAAGAGAGATTTTAGAAAAAGTAAATCAGGATTAGAAAAGGTTAAA	1020
DB		
2004	GAATATCTTTAAGAGCAATTTCTAAATTTTGAAGAAATTAAGAGTACATCAGTTACAGTCAG	2063
QY		
1021	GAATATCTTTAAGAGCAATTTCTAAATTTTGAAGAAATTAAGAGTACATCAGTTACAGTCAG	1080
DB		
2064	TAA 2066	
QY		
1081	TAA 1083	
DB		

RESULT 3  
AAx61816  
ID AAX61816 standard; DNA; 979 BP.  
XX  
XX  
AAX61816;  
XX AC  
XX DT  
19-JUL-1999 . (first entry)  
XX DE  
B. burgdorferi antigenic protein coding sequence, t51-2.nt.  
XX  
XX  
antigenic protein; vaccine; Lyme disease; infection; detection; ss.

OS	Borrelia burgdorferi.	
XX		
XX		
PN	WO9859071-A1.	
XX		
XX		
PD	30-DEC-1998.	
XX		
XX		
PF	18-JUN-1998; 98WO-US012718.	
XX		
XX		
PR	20-JUN-1997; 97US-0050359P.	
PR	22-JUL-1997; 97US-0053344P.	
PR	22-JUL-1997; 97US-0053377P.	
PR	03-SEP-1997; 97US-0057483P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(MEDI-) MEDIMMUNE INC.	

XX Choi GH, Erwin AL, Hanson MS, Lathigra R;  
PI  
XX  
XX WPI; 1999-189980/16.  
DR P-PSDB; AAY20119.  
DR  
XX  
XX  
PT New isolated *Borrelia burgdorferi* nucleic acids - used to develop  
PT products for the diagnosis, prevention and treatment of diseases caused  
PT by *Borrelia*, particularly Lyme disease.  
XX  
XX  
PS Claim 1: Page 204; 275pp; English.

XX This sequence encodes a Borrelia burgdorferi (Bb) protein of the  
CC invention, which is suitable for use in a vaccine. The Bb polypeptides  
CC can be used in vaccines for eliciting protective antibodies to members of  
CC the Borrelia genus, particularly for the use against Lyme disease in  
CC humans and animals. They can be used for preventing or attenuating an  
CC infection caused by a member of the Borrelia genus. The products can also  
CC be used for detection of members of the Borrelia genus  
XX  
XX Sequence 979 BP: 490 A; 86 C; 211 G; 192 T; 0 U; 0 Other;  
SO

	Query Match	39.4%	Score 979	DB 2	Length 979
	Best Local Similarity	100.0%	Pred. No. 4e-122		
	Matches 979	Conservative	Mismatches 0	Indels 0	Gaps 0
QY	1085	TTGCAAGATTGTATGCAACTGGTTAAAGATGCAACTGGTTAAAGATGCAACTGGTTAAAGATGC	1144		
Dh	1	TTGCAAGATTGTATGCAACTGGTTAAAGATGCAACTGGTTAAAGATGCAACTGGTTAAAGATGC	60		

QY	1145	ACTCGTTAAGATGCAACTGGTAAAAATGCAGAA	CAAAATATATAAAGGGGAAAAGTTC	CAAGG	1204
DB	61	ACTCGTTAAGATGCAACTGGTAAAAATGCAGAA	CAAAATATATAAAGGGGAAAAGTTC	CAAGG	120
QY	1205	ATTTTTAGAAAAGATTTTAGATCCAGTAAAGGATA	AAAAATGCTTCAAATGGTCCAATAGC	1264	
DB	121	ATTTTTAGAAAAGATTTTAGATCCAGTAAAGGATA	AAAAATGCTTCAAATGGTCCAATAGC	180	
QY	1265	AGATGAATTTGGCAAAAAAATTTACAGAA	GAGAAAGGTAAATAACGGCGGAAGAGAAA	1324	
DB	181	AGATGAATTTGGCAAAAAAATTTACAGAA	GAGAAAGGTAAATAACGGCGGAAGAGAAA	240	
QY	1325	TGATAAGCTGCTCTTTTATAGGAGAAGAACT	CAAAAGAGGATGAAGAAAGAAATCAGCAAGC	1384	
DB	241	TGATAAGCTGCTCTTTTATAGGAGAAGAACT	CAAAAGAGGATGAAGAAAGAAATCAGCAAGC	300	
QY	1385	TGTTAAATTTAGAAAGAAAAAATCCGAAGAGGATA	AGAAAGTTGTTAAATTTAGAAAGGAA	1444	
DB	301	TGTTAAATTTAGAAAGAAAAAATCCGAAGAGGATA	AGAAAGTTGTTAAATTTAGAAAGGAA	360	
QY	1445	AGAAATTTAGAAGTTAAAAAGAGACTGAGAGAGAT	GAAATATAAGAGAAATATAGAGAAACA	1504	
DB	361	AGAAATTTAGAAGTTAAAAAGAGACTGAGAGAGAT	GAAATATAAGAGAAATATAGAGAAACA	420	
QY	1505	AAAAACAAGAGTGGAAAAAGCACAGAAGAAAGAA	CAACGACAAGAAAGAAACGAAA	1564	
DB	421	AAAAACAAGAGTGGAAAAAGCACAGAAGAAAGAA	CAACGACAAGAAAGAAACGAAA	480	
QY	1565	AAAAACAAGACACAGAAGAAAAAGAAACGAA	AAACGACAAGAAAGAAAGAAACGAG	1624	
DB	481	AAAAACAAGACACAGAAGAAAAAGAAACGAA	AAACGACAAGAAAGAAAGAAACGAG	540	
QY	1625	AGCTAAAAACAAATTTAAAAAATCTCGGAT	AAAAATAGATAGATAAGTTGGAATATTGA	1684	
DB	541	AGCTAAAAACAAATTTAAAAAATCTCGGAT	AAAAATAGATAGATAAGTTGGAATATTGA	600	
QY	1685	TGGTATAGAAGTCAAAACAAGTGTAAAAACG	AAAGCAAGTTATAGATAAAATTCGGGGCC	1744	
DB	601	TGGTATAGAAGTCAAAACAAGTGTAAAAACG	AAAGCAAGTTATAGATAAAATTCGGGGCC	660	
QY	1745	TGTTATAGATTTTACCGATGACACAAAAAAG	CTATATATAAAACATGGGGAGATTT	1804	
DB	661	TGTTATAGATTTTACCGATGACACAAAAAAG	CTATATATAAAACATGGGGAGATTT	720	
QY	1805	AGAGATGAAGAGGCGAAGGATTTGGGAAAT	TATTTCAAGAAATGAGTGATCTAGAGA	1864	
DB	721	AGAGATGAAGAGGCGAAGGATTTGGGAAAT	TATTTCAAGAAATGAGTGATCTAGAGA	780	
QY	1865	TGAGTTAAGAACCAAAATTTAAATAAGATA	TATAAAAAATTTATGCCCATGAAAATGAGCC	1924	
DB	781	TGAGTTAAGAACCAAAATTTAAATAAGATA	TATAAAAAATTTATGCCCATGAAAATGAGCC	840	
QY	1925	TCCTCTAAAAAGAAATGTAGATGTCACG	GAATTAAGAGAGATTTAGAAAAGTATAAATC	1984	
DB	841	TCCTCTAAAAAGAAATGTAGATGTCACG	GAATTAAGAGAGATTTAGAAAAGTATAAATC	900	
QY	1985	AGGATTTAGAAAAGGTTAAAGAAATCTTAA	GACAAATCTTAAATTTGAAGAAAATTAAGG	2044	
DB	901	AGGATTTAGAAAAGGTTAAAGAAATCTTAA	GACAAATCTTAAATTTGAAGAAAATTAAGG	960	
QY	2045	ATACATCAGTTACAGTCAG	2063		
DB	961	ATACATCAGTTACAGTCAG	979		

RESULT 4	
AAx20252/c	
ID	AAx20252 standard; DNA; 35515 BP.
XX	
AC	AAx20252;
XX	
DT	04-MAY-1999 (first entry)

XX DE Borrelia burgdorferi polynucleotide sequence #5.  
XX KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
XX KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
XX KW infection; diagnosis; characterisation; detection; ds.  
XX OS Borrelia burgdorferi.  
XX PN WO9858943-A1.  
XX PD 30-DEC-1998.  
XX PF 18-JUN-1998; 98WO-US012764.  
XX PR 20-JUN-1997; 97US-0050359P.  
XX PR 22-JUL-1997; 97US-0053344P.  
XX PR 22-JUL-1997; 97US-0053377P.  
XX PR 03-SEP-1997; 97US-0057483P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PA (MEDI-) MEDIMUNE INC.  
XX PI Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
XX PI Smith HO;  
XX DR WPI; 1999-081217/07.  
XX PT New isolated Borrelia burgdorferi nucleic acids - used to develop  
XX PT products for the detection, diagnosis, characterisation, prevention and  
XX PT therapy of infections, particularly Lyme disease.  
XX PS Claim 1; Page 831-851; 1128pp; English.  
XX CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
XX CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
XX CC detection, diagnosis, characterisation, prevention and therapy of Bb  
XX CC infections, e.g. Lyme disease. They can also be used for the production  
XX CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of  
XX CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
XX CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
XX CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
XX SQ Sequence 35515 BP; 10795 A; 5947 C; 4439 G; 13907 T; 0 U; 427 Other;

Query Match 36.9%; Score 917.2; DB 2; Length 35515;  
Best Local Similarity 66.9%; Pred. No. 5.9e-114;  
Matches 1355; Conservative 20; Mismatches 623; Indels 26; Gaps 5;

QY 1 ATTATTATACAGAAACCCCTGACTTTTTCAGAGAGATTTTGAATTTTATAGAAATATGGA 60  
DB 11145 ATTATTAGCAGAAACCCCTGATTTTTRAGAGATTTTAAATTTTATAGAAATATGGA 11086  
QY 61 TAAATGCTAATTTGGTTGCTTTTAAACTTATGTTGGATTTTGAATAAATAAGTACGTC 120  
DB 11085 TAAATGCTAATTTGATTTATCTTTAAATTTATGTTGGTTTTCGAAAGTARGTACGCC 11026  
QY 121 TTGTATCAAGATTTTCTCATTAATAATGATTTTGTGCTGCTGTTGGATAGCCTCGAACT 180  
DB 11025 KTGAGTCRAGATTTTCTCATTAAGTAAATTTTCGTGAGCTTTTGAATAGCCTCAAT 10966  
QY 181 CTTCTGAGTTGATAACAATTTCTTAATAACAAGTACATTTCTTTTTCACCATTTA 240  
DB 10965 CTTTCAGATTTGATGACATTTCTTAATCAAGTCAATTTCTTTTTCAGTAYATTTA 10906  
QY 241 CTTTATGTTGTATAAGTTTTCATTTTTCATTTTTCCTTAATAAAGCTTGAATATCTTCATTT 300  
DB 10905 CTTTATATGTAARAAGTTTCTCCAGTTTGTGTARTAGMGGRGTAATATCTTCGATTT 10846  
QY 301 TTACTTTTTCAGTTGGTGGCCCTGCAGCCACTTATTTCGAGTAAATGTAAAAACCAAC 360  
DB 10845 TWACTTTTGAATTTCKGCMCCCTCCACCCACTTATTTCGAGTAGATGTAGAAACCAAC 10786

QY 361 CAGATATTGGATCAGCTTGTTTAAAGATTTTGTGATCATTTTCAATAGTTTGCATTT 420  
DB 10785 CAGAAATWGGGTGCARTTTTAAATGTTTTRACGCATTTTCAATATTTTGTCTACTTT 10726  
QY 421 TTGGGTCCTCAATPAAATTTAGGAGTTGGCTTTGAAGCTTTTGTAGTGGCTTAGAAGAAA 480  
DB 10725 TTGAGGTTAAATAAAACTTAGGAGTTGGTTTGAAGCTTTTGTAGTGGCTTAGAAGAAA 10666  
QY 481 TTTTGTAGTGAATTTTAAAGATTTTGTGTTTCATTTTATTTAGTTTGTAGTGAATCTGTATA 540  
DB 10665 TTTTGTAGTGAATTTTAAAGATTTTATTTTTCATTTTACCACATTTTGTAAATCTTGAATA 10606  
QY 541 ATTTAAGCATAAATCTATGTTGAAATTTTAAATTAAGATAATTTATTTTCATGTCCTATA 600  
DB 10605 GTTTCAGCATAAATCCATATTGAAATTTTAAATTAAGATAATTTATTTATATATCCATA 10546  
QY 601 AATCCCTCCTTATAAGTGTACTTTTAAATTAAGTAAAGATAATAAATTTGATTAATA 660  
DB 10545 AATCCTCCTTAGAAGTGTTACTTTTAAATTAAGTAAAGATAATAAATTTTAAATA 10486  
QY 661 ATGTAAATTTATTTTACCAAAACCAAAATTTAGTCAAAATTTGTGGCTTCTCATTTG 720  
DB 10485 ATGTAATTTATTTTATCAAAACCTTAAATTTTGTCAAAATTTTGGGTGTTCTCATTTG 10426  
QY 721 CATGCAAAATTTGGATTTGTAGGATGTGATATAACAGAGAGCAATTTTAAAGGGGT 780  
DB 10425 CATGCAAAATTTGGGTGTTGTGAGTGGCTGTGATATAACAGAGATTTTTCAGGGGTG 10366  
QY 781 GCACCTTAAGAAGATACATCTTAAAGTGATATATAGCAAGACTTTGAAATTTTAACTT 840  
DB 10365 TCGATATAAGAAGACAGTATCTTTATCTAATATATAGCAAGACTTTTGAATTTTAACTT 10306  
QY 841 GTATGTGTTTGTAGTCTTTTATATAGCAGGGCCATTTGCAATGGAGAGATTTTATAGGGA 900  
DB 10305 GTATGGATTTTGTAGTCTTTTGTAAATGAGTGGTGCATTTGCAATGGAGAGATTTTGGGA 10246  
QY 901 GTTCATTAATAATTTATTTGGCTTTGTGTTTAAATTAAGTAAATTTGATGTAATAAATTTAT 960  
DB 10245 GTTGTGTTAAATTTATTTTGGCTTTTGTGTTTAAATTTGATGTAATAAATTTTAT 10186  
QY 961 ATATTTAAATCTTTGAAAAATTTGTAATTTGTTGGGTTGTGTAATCTTAAAGCTTAT-G 1019  
DB 10185 ATATTTAAATCTTTGAAAAATTTGTAATTTATAGCAATTCGTTAGATCTTAAGGATTTAG 10126  
QY 1020 GAGTGGATTAATAAATAAATAAATAATTTATTTATTTTGTGCTGTATTTGTGCTGATA 1079  
DB 10125 GAGTAACCTTATGAATAAAGAAATGAAATGTTTATTTATTTGTGCTGTATTTGTGCTGATA 10066  
QY 1080 AGTTCTTTCGAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAA 1139  
DB 10065 ATTTCTTTCGAAGATTATGCAAGTGGTAAATCTAATAAATTCAGA-----ACAA 10015  
QY 1140 GATCAACTGGTAAAGATGCAACTGGTAAATCTGTAATAAATAAATAAATAAAGGGAAGTT 1199  
DB 10014 AATCTAGAAAGTTTCAGAAACAAATGTAATAAATAAATAAATAAAGGGAAGTT 9955  
QY 1200 CAAGGATTTTATAGAAAGATTTTATAGTCCAGTAAAGATTAATTTGCTTCAATTTGCTCA 1259  
DB 9954 GAAGGATTTTATAGAAATTTTATAGTCCAGTAAAGATTAATTTGCTTCAATTTGCTCA 9895  
QY 1260 ATAGCAGATGAATTTGGCAAAATAAATAAATAAAGGTAATAAATAAAGGGAAGAA 1319  
DB 9894 AAAGAAATTTGAAA-----ACAAATTCAGAAATTAAGATTAATAAATAAAGGGAAGAA 9847  
QY 1320 GAAATGATAAGCTGCTTTTATAGGAGAGATTAATAAAGGATTAAGAGAAATTTAG 1379  
DB 9846 TTAGATTTTAAAAAATCTCTATTGAACATATTCTGAGTATGAAGAAAAATAAATAA 9787  
QY 1380 CAAGCTGTTAATTTAGAAAGAAAAATCGGAAGAGATTAAGAAAGTTGTTTAAATTTAGAA 1439  
DB 9786 ATAAAGAAAAATTTGAAGGAAAGGACTTTGAAGATTAATTTAAGGAGCTTTGAAGAGAT 9727  
QY 1440 GAGAAAGATTTAGAGTTAAAAAGAGACTGAAAGAGATGAAGATAAAGAAAGAAATAGAG 1499

9726 TTAGCAAAAGAAAAGGGGAGAGAAAAAAGCTTTTACAAGAGGCCAAAACAGAAATTTGAA 9667

1500 AACAACAAAACAGAGCTGGAAAAGCACAAGAAGAAACACAGACAGAAGAAAAAGAAA 1559

9666 GAATATAAAAAACAAGTAGATCTTCAACTGGGAAACTCAGCGCAGAGGCTTAAAAAC 9607

1560 CGAAAAAAAACAAGAACAGCAAGAAGAAAAAGAAAACGAAAAACGACAGAACAAGAAAAAGAA 1619

9606 CGAGGTGGTGTGGAGTGCAGAGCTGCGCAATGAAATAGGTTTGGGTGTAAGT 9547

1620 AGAGAGACTTAAAAACAAAATTAACAACTTGGCGATAAATAATAGATGAGATAAGTTCGAAT 1679

9546 TATTCTAATGGCGCAGTGAACAACAGCAATACCTGATGAATTTAGCAACAAGTTTAGAT 9487

1680 ATTGATGGTATAGAAAGTCAAACAAGTGTAAAAACCGAAACAGCTTATAGATAA--AATTA 1737

9486 GATTCCTTTAAAAGATTGAAGAAGAACTTAAGCGAATACAGAAGATAAAAAAGAAATAA 9427

1738 CGGGCGCTGTATAGTATTTTACCAGTGCACAACAAAAGCTATATATAAACATGGG 1797

9426 CAGTGGTATCTTTTAAAGATAGAAATTCAAAACCAAGGAGAGAAAACAAAAGATGTGAATAAA 9367

1798 GAGATTTAGAAAGATGAAGAAGCGCAAGGATGGGAAAAATTTATGAAAGAAATTCAGTGTATA 1857

9366 AAAATATTGATTATTTTGTGTTTTTGCACCTATATATTTCTGTAAAAATTT--ATGCAA 9309

1858 CTAGAGATAGGTTAAGAACCAAAATTAAATTAAGATAATAAAAAATATTATGCCCATGAAA 1917

9308 CTGGTAAGATATAAAAAACAAATGCAAAAGGGAATAATTTAAAGGATTTTTTATAGATAAGTTT 9249

1918 ATGAGCCTCTCTCAAAAAGAAAAATGTAGATGTCAGCGAAATTTAAAGAAAGATTTAGAAAAAG 1977

9248 TAGATCCGCAAAAGATATAAATTTACTTCAAGTAGTTCAAAAGTAGATGAATTAGCAAAA 9189

1978 TAAAAATCAGGATTAGAAAAGGTTAAAGAAATCTTTAAAGCAAT 2021

9188 AATTACAAAGAAGAGATCAAGATAATGAAATTAATGAAATTAATGCGAGGCGAT 9145

RESULT 5	
AAX20292/c	
ID AAX20292 standard; DNA; 2892 BP.	
XX	
XX AAX20292;	
XX AC AC	
XX XX	
DT 04-MAY-1999 (first entry)	
XX	Borrelia burgdorferi polynucleotide sequence #45.
DE	
XX	
XX Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;	
KW KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;	
KW infection; diagnosis; characterisation; detection; ds.	
XX	
OS Borrelia burgdorferi.	
XX	
XX WQ958943-A1.	
XX	
PD 30-DEC-1998.	
XX	
PF 18-JUN-1998; 98WO-US012764.	
XX	
PR 20-JUN-1997; 97US-0050359P.	
PR 22-JUL-1997; 97US-0053344P.	
PR 23-JUL-1997; 97US-0053377P.	
PR 03-SEP-1997; 97US-0057483P.	
XX	
PA (HUMA-) HUMAN GENOME SCI INC.	
FA (MEDF-) MEDIMMUNE INC.	
XX	
PI Fraser C. White OR, Clayton R, Dougherty BA, Lathigra R;	
PI Smith HO;	
XX	

DR	WPI; 1999-081217/07.	
XX	New isolated <i>Borrelia burgdorferi</i> nucleic acids - used to develop	
PT	products for the detection, diagnosis, characterisation, prevention and	
PT	therapy of infections, particularly Lyme disease.	
XX	Claim 1; Page 1018-1019; 1128pp; English.	
XX	AAX20248 to AAX20402 represent polynucleotide sequences isolated from	
CC	<i>Borrelia burgdorferi</i> (Bb). Products derived from Bb can be used for the	
CC	detection, diagnosis, characterisation, prevention and therapy of Bb	
CC	infections, e.g. Lyme disease. They can also be used for the production	
CC	of biosynthetic products, e.g. enzymes. <i>Borrelia</i> belongs to a family of	
CC	motile, spiral-shaped bacteria called Spirochetes. Spirochetes are a	
CC	pathogenic in humans and <i>Borrelia</i> causes epidemic and endemic relapsing	
CC	fever, and Lyme borreliosis, more commonly known as Lyme disease	
XX	Sequence 2892 BP; 870 A; 518 C; 304 G; 1200 T; 0 U; 0 Other;	
XX	Query Match 33.3%; Score 827.4; DB 2; Length 2892;	
XX	Best Local Similarity 62.4%; Pred. No. 6.3e+102;	
XX	Matches 1795; Conservative	
QY	150 TTTTTCGTGCTGTTGGATAGCCTCGAACTCTTCGTAGTGTGATACAAATTCCTTAATA	209
DB	2892 TTTTTCGTGAGCTTTTTCGAATAGCATCAAAATTCACAGATTTTATGACAAATTTCTTAATG	2833
QY	210 CAAGTTACATTTCTTTTTCCTTTTTCGCACATTTACATTTTATGTTGTTATAAGTTTTCCATTT	269
DB	2832 CAAGTACACATTTCTTTTTCCTTTTTCGTGACATTTACATTTTATATGTTATAAAGTTTCTCAGTT	2773
QY	270 TTGCTTAAAAAAGTTCGAAATATCTTGCAATTTTACATTTTTCAGTTTCGGTCCCTTCGAG	329
DB	2772 TTGCTTAAAAAAGGAGTAAATATCTTGCAATTTTACATTTTTCAGCTCGGCACCTCTGCAG	2713
QY	330 CCACCTATTTCGGAGTAAATGTTAAAAACCAACACAGATATTCGATCAGCTTCTTTAAGAGTT	389
DB	2712 CCACCTATTTCGGAGTAAATGTTAAAAACCAACACAGAAATTCGGTCAATTTATTTAATGTT	2853
QY	390 TTGATGCATTTTCAATTAGTTTTCGCAATTTTTCGGGTCAAAATAAAATTTAGGAGTTGGC	449
DB	2652 TTAAACATTTTTCATTTATTTTGATTAATTTTTCGATTCAAATAAAACTTTGGAGTTGGT	2593
QY	450 TTTTCAAGCTTTTTCAGTTCCTTAGAAGAAATTTTTCAGTCAAATTTTAAAGATTTTCTTT	509
DB	2592 TTTTGAAGCTTTTTCAGTTCCTTAGAAGAAATTTTTCAGTCAAATTTTAAAGATTTTCTTT	2533
QY	510 TCATTTATTAGTTTTCAGTTCCTTAGAAGAAATTTTTCAGTCAAATTTTTCAGTCAAATTT	569
DB	2532 TCATTTAATACATTTTCAGTTCCTTAGAAGAAATTTTTCAGTCAAATTTTTCAGTCAAATTT	2473
QY	570 TTTTAAAAATAAGATAAATTTATTCATGTCATAAAAATCCCTCCTTATAAGTGTACTTTTAA	629
DB	2472 TTTTAAAAATAAATTTATTTAGTATCCATAAAATCCCTCCTTTGGAAGTGTACTTTTAA	2413
QY	630 ATTAAAGTAAAGTAAATAAAATTCATTTAAATAATGTTATTTATTTTACCAAAACAAAA	689
DB	2412 ATTAAAGTAAAGTAAATAAAATTTAAATAAATGTTATTTATTTATTTTAAACCCCTAA	2353
QY	690 AAATTTAGTCAAATTTGTCGCTCTCTCATTCGATGCAAAATTTGGATGTAGAGTAGCTG	749
DB	2352 AAATTTAGTCAAATTTATGTTGTTCTCATTCGATGCGAAATTTGGGTGTGAGGTGGCTG	2293
QY	750 TGATAAACAAGAGGCAATTTTTCAGGGGTGCATTTAAGAAACATCTATACCTTTAAGT	809
DB	2292 TGATAAACAAGAGGCAATTTTTCAGGGGTGGACCTTAAGAAACATCTATACCTTTAAGT	2233
QY	810 GATATATAGCAACACCTTTGAAATTTTAAAGTTGTTATGTTTGTAGTCTTTTATAAATGAG	869
DB	2232 GATATATAGCAACACCTTTGAAATTTTAAAGTTGTTATGTTTGTAGTCTTTTGTAAATGAG	2173
QY	870 CAGGCCCATTTGCAATGAGAGATTTTAGGGAGTTGATTAATAATTTATTTTCGGTTTCTTT	929

Db 2172 CCGGGCATTGTCAAATGGAGAGATTTTGGGAGTTGGTTAAAAATTACATTTGAGTTTGT 2113  
Qy 930 AATATGTAAATAGCTGAATGTAAACAAAATTATATTTAAATCTTTGAAAAATTTGTAATG 989  
Db 2112 AATATGTAAATAGCTGAATGTAAACAAAATTATATTTAAATCTTTGAAAAATTTGTAATG 2053  
Qy 990 TTTGGGGTTGTGTAAACCTTAAGCTTATGGAAGTATGGAATGAAATGAAATGAAATG 1049  
Db 2052 TTAGCTGTGTGTATGATTTAGGACTTATGGGAAATTTATGAATTAAGAAATGAAATG 1993  
Qy 1050 TTTATTTATTTGCTGTATTTGCTGTATGATTAAGTTCTTGAAGATTTGATCAACTGTTAA 1109  
Db 1992 TTTATTTGTTGCTGTATTTTATCTTATAGTGTCTTGCATAATTTCTATCTCATATGAT 1933  
Qy 1110 GATGCAACTGGT----- 1121  
Db 1932 GAGCAAAAGTAGTGGTGAGATAAAACCATCTTTTATATGATGAGCAAAAGTAATGTTGAGTTA 1873  
Qy 1122 ----- 1121  
Db 1872 AAACCTTAAAAAATAGAAATTCCTAAATTTACTGTAAAAAATTAAGAAATTAATAT 1813  
Qy 1122 ----- AAAGATGCAACTGGTAAAGATGCA 1145  
Db 1812 AGTAACTGGACAGACCTAGGAGATTTAGTTGTAAAGAAAGAGAAAAATGTTATGATACG 1753  
Qy 1146 ACTGTTAAAGA----- 1156  
Db 1752 GGTTTAAACGCTGGGGACATTCGGCTACATCTTTTTCATTAAAGAANTCAGAAGTTAAT 1693  
Qy 1157 ----- 1156  
Db 1692 AACTTTTAAAGCAANTGACTAAAGCGGATCATTTAAACCTAGTTTGTATTATGATAT 1633  
Qy 1157 ----- 1156  
Db 1632 AAGTACGAAACAAAGTAGTCAAAATGGTATCCAAAAACAAAGAGATCATAAACAAAAATAGAA 1573  
Qy 1157 ----- 1156  
Db 1572 AGTATTANTGGTCTGACACATATTGCGTTTTTAGGAGATAAAATTAATTAACGGTGTGGG 1513  
Qy 1157 ----- 1156  
Db 1512 GGAGATAAAACAGCTGAATATGCAATACCACTAGAAAGTGTAAAAAATTTAAAAATAG 1453  
Qy 1157 ----- 1156  
Db 1452 AATTTAGAAATATAGGAGAGATAATATGCAATAAAAAACAATTTGATTTTGTGCTGTT 1393  
Qy 1157 ----- TGCAACTGGTAAAAATGCAGAACAAAAATATA 1187  
Db 1392 TTTGCGCTGATAATTTCTTGCAAGAATTTTGCNACTGGTAAAGATATAAAACAAATTTCA 1333  
Qy 1188 AAGGGAAGTTCAAGATTTTGAAGAAATTTTAGATCCAGTAAAGGATAAAATTTGCT 1247  
Db 1332 GAAGGGAAAAATTAAGAGATTTGTAATAAGATTTTAGATCCAGTAAAGGATAAAATTTGCT 1273  
Qy 1248 TCAAAATGGTCCAATAGCAGATGAATTTGGCAAAAAAATTTACAAGAGAAAGAAAGTTAAT 1307  
Db 1272 TCAAGTGGTACAAAAGTAGTAGTAGCAAAAAAATTTACAAGAGAAAGAAAGAA 1213  
Qy 1308 AACGGGAAGAAG----- 1320  
Db 1212 TTAATGCGGGCGATGATCCTAATGGCAGTGGAAATAATCCGCCACAGTATTGCGGGAA 1153  
Qy 1321 ----- AAAATGATAAGCTGTCTTTTTAGGAGAGAGATCAAAAGAGATCAAGAGAA 1373  
Db 1152 AATATTCAAAATAGTATTGATTTAAAGCAATTAAGAACAAAGTATGTTGTTCAACAGAA 1093  
Qy 1374 AATGAGCAA-----GCTGTATTTTAGAAGAAAAAATCGCGAAGAGGATAAGAA 1424  
Db 1092 AAAAAAGTAGAAGAGCTGAAGCTAAAGTTGAAGAAAAATAAGAAAAACCAAGAGAAATACA 1033

RESULT 6

AA20285/c

ID AA20285 standard; DNA; 3129 BP.

Qy 1425 GTTGTAAATTTAGAGAGAAAAAATTGAAGCTTTAAAAAAGAGACTGAAGAGATGAAGAT 1494  
Db 1032 GAAGAAAACATTAAAGAAAAGAAATATATGACGAAACAAAACAACAGATTTAGCTAAA 973  
Qy 1485 AAAGAGAAATAGAGAAACAAAACCAAGAACTGGAAAGAACACAAAGAAAGAAACAA 1544  
Db 972 GCTAAGAGAGAGAAACCAACAAAAAGAACAAAAAGACATCAAGAGAGAGCAACAAAGAAA 913  
Qy 1545 CAAGAGAAAAAGAAACGAAAAAACAAGAACAGCAAGAGAAAAAAGAAACGAAAAACGACAA 1604  
Db 912 GCTAAGACAGAAAAAGAAAAAGAGAAAGAGAGCGCAGAACAAACAAACGACAA 853  
Qy 1605 GAACAAAGAAAGAAAGAGAGACTTAAACAAAATTTAAAAAATTTGGGATAAATAGAT 1664  
Db 852 GAAGAGGAAGAAAAAAGGCAAGTTGATAACCAAAATTTAAACACCTTATAGCTTAAATAGAT 793  
Qy 1665 GAGATTAAGTTGGAATATTGATGTTATAGAAAGTCAAAACAGTGTAAACCGAAGACAGTT 1724  
Db 792 GAGATCAATGAATATTGATGTTTAAATGGCAACGACTGTAGGCCCAAGGCGTT 733  
Qy 1725 ATAGTAAATTTACGGGCTGTATATGATTTATTTTACCGATGACAAACAAAAAGCTATA 1784  
Db 732 ATAGATAGATTTACTGGGCTGTGTATGATGATTTTACCAATGGCAATATTTCTATACGC 673  
Qy 1785 TATAAACATCGGAGATTTAGAGATCAAGAGCGCAGAGATTTGGGAAATTTATTGAAA 1844  
Db 672 GAACTTGGGAGGGTTAGAAAGGAATCAGAAACGAGAGATTAGGAAATTTATTGAAA 613  
Qy 1845 GAAATGAGTGATCTAGAGATGAGTTAAGAACCAAAATTAATAAAGATAATAAAAAATAT 1904  
Db 612 GAAATGAGTGATCTAGGAGCGCTAAGAACTAAATTAATGAAGCAATAAACCATAT 553  
Qy 1905 TATGCCATGAAATAGAGCTTCTTAAAGAAATGTAGATGTACAGGAAATTTAAAGAA 1964  
Db 552 ACTGGTTACGAA--GAGCCTAAGTTAAAGAAAGTGTAAATGTTAGCGAAATTTAAAGAA 496  
Qy 1965 GATTTAGAAAAAGTAAATCAGGATTTAGAAAGGTTAAAGAAATCTTTAAAGACAAATCT 2024  
Db 495 GATTTAGAAAAATTAATTAATTAATTAAGAGAGTTTAAAAAAATCTTTAAAGATAGTTCT 436  
Qy 2025 AAATTTGAAGAAATTTAAAGGATACATCAGTTTACAGTCAGTAAATTTATTTGATCTTTTA 2084  
Db 435 AAATTTGAAGAAATTTAAAGGATACATCAGTCAGTACAGTAAATTTATTTGATGCTTTTA 376  
Qy 2085 GATGTAACTAAATTTTACGTACACAAAATACAGCTAGTAGAAAGTTTCACTGGCTGTTA 2144  
Db 375 GGTGTAACTAAA-TTTCGCTATACAAAGTACAGCTAGTAGAAAGTTTCACTGGCTGTTA 317  
Qy 2145 TTTTTTTGATGATTTCAATTTGTTATGAATATAGAAATGTTTTCTATCAAACTTTTCAITTA 2204  
Db 316 TTTTTTTGATGATTTCAATTTGTTATGAATATAGAAATGTTTTCTATCAAACTTTTCAITTA 257  
Qy 2205 AAAAGTG-CAAAAATATGCTAAAAATGTTGTTTTTATATCTCTAGAGCTATGA 2263  
Db 256 AAAAATGCCAAAACTATGCTCAAAAATTTGTTTTTATATCTATCTATATAATTAATA 197  
Qy 2264 CGTATACAAATCAGATTTTCAATTTTGTATGATAATTTATATAAGAAAAACAAAAAGAAA 2323  
Db 196 TGCATCTAATGAATTTCAANTTTTTATGATATCTTAGTGAGATTTAAAAAGTCAA 137  
Qy 2324 TAGATAAATCTTATAAACAAGCTCTATTTAACTAGCCNAAATAACTCTTAAAGCAAAAAAGAC 2383  
Db 136 TAAATAAACTT-----TATGAAACCGAACCAAGCAACCGCAAGAAACAAAAAGTC 89  
Qy 2384 AAATNTACAGTCGTGTTGAAGAGATGCAAAAAATCGTAATAAAAAACGGAAG 2438  
Db 88 AAATGTATAGCTCTTATTAAGCAGCGCAAGATACGGAATAAAAAATCTGGAAAAAG 34

XX AC AAX20285;  
 XX DT 04-MAY-1999 (first entry)  
 XX DE Borrelia burgdorferi polynucleotide sequence #38.  
 XX KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
 XX KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
 XX KW infection; diagnosis; characterisation; detection; ds.  
 XX OS Borrelia burgdorferi.  
 XX PN WO9858943-A1.  
 XX PD 30-DEC-1998.  
 XX PF 18-JUN-1998; 98WO-US012764.  
 XX PR 20-JUN-1997; 97US-0050359P.  
 XX PR 22-JUL-1997; 97US-0053344P.  
 XX PR 22-JUL-1997; 97US-0053377P.  
 XX PR 03-SEP-1997; 97US-0057483P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PA (MEDI-) MEDIMUNE INC.  
 XX PI Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
 XX PI Smith HO;  
 XX DR WPI; 1999-081217/07.  
 XX PT New isolated Borrelia burgdorferi nucleic acids - used to develop  
 XX PT products for the detection, diagnosis, characterisation, prevention and  
 XX PT therapy of infections, particularly Lyme disease.  
 XX PS Claim 1; Page 1004-1006; 1128pp; English.  
 XX CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
 XX CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
 XX CC detection, diagnosis, characterisation, prevention and therapy of Bb  
 XX CC infections, e.g. Lyme disease. They can also be used for the production  
 XX CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of  
 XX CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
 XX CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
 XX CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
 XX SQ Sequence 3129 BP; 1067 A; 566 G; 286 G; 1210 T; 0 U; 0 Other;  
 Query Match 31.5%; Score 784; DB 2; Length 3129;  
 Best Local Similarity 64.9%; Pred. No. 3.8e-96;  
 Matches 1272; Conservative 0; Mismatches 650; Indels 38; Gaps 6;  
 94 TGAATTTTCAAAAATAAGTACGCTCTGTATCAAGATTTTCTCAATTAATAATGATTTT 153  
 3129 TGTCTTTTGGAAAAGATAAGTACGCTTGTGATCAAGATTTTCTTGGAAATGATTTT 3070  
 154 TGTGTGCTGTTTGGATAGCTCGAATCTTCTGAGTTGATACAAATTTCTTAATACAAG 213  
 3069 TATGTGCTGTTTGGATAGCTCGAATCTTCTGAGTTGATGACAATTTCTTAATACAAG 3010  
 214 TTACATTTCTTTTTTGGCACAATTTACATTTTATGTTGATATAAGTTTTCATTTTGGC 273  
 3009 AGGTAATTTCTTTTTTGGCACAATTTTACTTTTAAATAGTATATAAGTTTTCGGGTTTGC 2950  
 274 TTAATAAAGTTGAATAATCTTGCAATTTTACTTTTTTTCAGTTTCGGTGCCCTGCGAGCCAC 333  
 2949 TTAATAAAGTTGAATAATCTTGCAATTTTACTTTTTTTCATTTTTCAGTTTCCTACATCCAC 2890  
 334 TTATTGGAGTAATGTAAACCAACCAAGATTTGAGTACAGTTGTTTAAAGATTTTGA 393  
 2889 TTATTAAAGTAGATGCACAAACCAACCAAGATTTGGGTCAATTTGTTTAAAGGTTTGG 2830

QY 394 TGCATTTTCAATTAGTTTGCCTCAATTTTGGGCTCAAAATAAATTTAGAGTTGGCTTTG 453  
 DB 2829 CACATTTTACAAATAATTTAAATACCTTTTAGGGGTTAAATAAAACCTTAGGAGTTGGTTTG 2770  
 QY 454 AAGCTTTTGTAGAGCTTAGAAGAAATTTTATAGTGAATTTTAAAGAAATTTTGTTCAT 513  
 DB 2769 AATTTCTTTTCTTTTACCTTTAGATGAATTTTATAGTGAATTTTAAAGAAATTTTGTTCAT 2710  
 QY 514 TTATTAGTTTTCATGATCTTGTAAATAATTAAGCATAAATCTATGTTGAATTAATTA 573  
 DB 2709 TTATTAGTTTTCATGATCTTGTAAATAATTAAGCATAAATCTATGTTGAATTAATTA 2650  
 QY 574 AATTAAGTAATTAATTCATGCTCCATTAATCCCTCTTATAGTCTTACTTTTAATTA 633  
 DB 2649 AATTAAGTAATTAATTCATGCTCCATTAATCCCTCTTATAGTCTTACTTTTAATTA 2590  
 QY 634 AGTAAAGTAATTAATTAATTCATGCTCCATTAATCCCTCTTATAGTCTTACTTTTAATTA 693  
 DB 2589 AGTAAAGTAATTAATTAATTCATGCTCCATTAATCCCTCTTATAGTCTTACTTTTAATTA 2530  
 QY 694 TTAGTCAAAATTTGTGGCTTCTCATTCATGCAATGCAAAATTTGGATTTAGGATAGCTGTGAT 753  
 DB 2529 TTAGTCAAAATTTGTGGCTTCTCATTCATGCAATGCAAAATTTGGATTTAGGATAGCTGTGAT 2470  
 QY 754 AACAGAAAGAGGCAATTTTAAAGGGTGCACCTTAAGAAAGATACTATCTTTAAAGTGA 813  
 DB 2469 AACAGAAAGAGGCAATTTTAAAGGGTGCACCTTAAGAAAGATACTATCTTTAAAGTGA 2410  
 QY 814 TATAGCAAAAGCTTTGAAATTTAAAGTTGATGTTTGTAGTCTTTTATTAATGAGCAGG 873  
 DB 2409 TATAGCAAAAGCTTTGAAATTTAAAGTTGATGTTTGTAGTCTTTTATTAATGAGCAGG 2351  
 QY 874 CCATTTCCAAATGAGAGATTTTAAAGGGTGCACCTTAAGAAAGATACTATCTTTAAAGTGA 933  
 DB 2350 GCATTTCCAAATGAGAGATTTTAAAGGGTGCACCTTAAGAAAGATACTATCTTTAAAGTGA 2291  
 QY 934 TGTAAATAGCTGAATGTAAACAAATTTATATTTAAATCTTTTGAAGAAATTTGATTTGTTG 993  
 DB 2290 TGTAAATAGCTGAATGTAAACAAATTTATATTTAAATCTTTTGAAGAAATTTGATTTGTTG 2231  
 QY 994 GGGTTGGTAAACTTAAGGCTTTTAAAGGGTGCACCTTAAGAAAGATACTATCTTTAAAGTGA 1052  
 DB 2230 GTGTTGGTAAATTTAGTACTTTTAAAGGGTGCACCTTAAGAAAGATACTATCTTTAAAGTGA 2171  
 QY 1053 ATTATTTGCTGTATTTTGTGCTGATAAGTTTCTTGAAGATTTGATGCAACTGCTTAAGAT 1112  
 DB 2170 ATTATTTGCTGTATTTTGTGCTGATAAGTTTCTTGAAGATTTGATGCAACTGCTTAAGAT 2111  
 QY 1113 GCACTGCTAAAGATGCACTGCTTAAGATGCACTGCTTAAGATGCACTGCTTAAGAT 1172  
 DB 2110 TTAAGAC--AAATGTAAAGAAAGAAAGTTTGAAGGATTTTATAGTAAAGGTTAAATGCA 2054  
 QY 1173 GCAGAACAAATATAAAGGGAAAGTTTCAAGGATTTTGAAGAAAGATTTTATAGTAAAGTGA 1232  
 DB 2053 GGTGACCATCTTAATACAGTCTGTTTAAATCCACCAGTATTTGCGGCAAGTTCCAC 1994  
 QY 1233 AAGGATAAATTTGCTTCAATGCTCAATAGCAGATGAATTTGCAAAATAAATTTACAGAA 1292  
 DB 1993 GATAACACACCCGTTATTAAGGGGCTTCAAGCAAGCAAGATGCTGCTCAAGCAAGCAAGAA 1934  
 QY 1293 GAAGAAAGGTAATTAACCGGGGAAGAAATTTGATAAGCTGCTCTTTTATAGGAGAA 1352  
 DB 1933 GAAGAAAGGTAATTAACCGGGGAAGAAATTTGATAAGCTGCTCTTTTATAGGAGAA 1874  
 QY 1353 TCAAGAGG-----ATGAGAAAGAAATTTGAGCAAGCTGTTAATTTAGAGAA 1400  
 DB 1873 TTAAGAGGCTAGAAAGAAATTTTCAAGATTTTAAAGAAATTTGAGCAAGCTGTTAATTTAGAGAA 1814  
 QY 1401 AAAATTCGGAGAGGTAAGAAATTTTAAATTTTGAAGAGAAAGAAATTTAGAGAA 1460  
 DB 1813 GAAAGTACTGAGAAAGTTTAAAGAAATTTGAGCAAGGAAATTTGAGCAAGGCTTTTAAAGTATGCT 1754  
 QY 1461 AAAGAGACTGAAGAGATGAAGATAAAGAAAGAAATTTAGAGAAACAAAGCAAGAGTGA 1520



Db 1753 AAAGATTGGTGTAAATGGAGTTATCTCTTAATGATGACTAATACTAATGATTTT 1694  
Qy 1521 AAACCAAGAAAGAAACACGACGAGAGAAAGAAACGAAAAAACAAGAACAGCAA 1580  
Db 1693 GTAAAAAGGTTATAGATGATGCTCTTAAATAATTTGAGGAAGAACTTGAAGCTAGCA 1634  
Qy 1581 GAAGAAAGAAACGAGACGACAGACAAAGAAAGAAAGAGAGAGCTAAACAAAT 1640  
Db 1633 GAGCTCAAAATATAGAGATATAAATAATTAATAAATAATGGGTTTGTAGTAGTAAATAAT 1574  
Qy 1641 AAAAATCTTGGGATAAATAGATGAGTAAATTTGGAATATTTGATGTATAGAAAGTCAA 1700  
Db 1573 AAACCAAGAACTAACATCAGTCTTATGTTTATTAGCATTTACATTTGCTGAAATTTAG 1514  
Qy 1701 ACAAGTGAACCAAGCAAGCTTTATAGATAAATTTACGGGCTCTGTATATGATTTT 1760  
Db 1513 GCAA---TAAAGCTAGGAGGGGATATGAAAAAATTTAGTCTGTTAATTTTGTGTTTT- 1458  
Qy 1761 ACCGATGACACAAAAAGCTATATATAAACAATGGGGAGATTTAGAGATGAGAGGC 1820  
Db 1457 -----ATTGTAGTAAGTTTAAGTCCAAATATAGAGAAATTTATACA 1415  
Qy 1821 GAAGGATTGGAAATTTATGAAGAATTTGAGTGATCTAGATGAGTTTAAAGAACAAA 1880  
Db 1414 GAAACTAAAGAGCTTTTCTAAAGAGATTTTAAACCTAATAATAAAGACTAGATAAT 1355  
Qy 1881 TTAATAAGATAATAAATAATTTATGCCCATGAAATGAGCTCTCTTAAAGAAAT 1940  
Db 1354 TATGATTTTAAATGAGTATGAAGAAAGTCACTTTTTCGATGCTCTCTAGAAATAGA 1295  
Qy 1941 GTAGATCTACGCGAAATTAAGAGATTTTAAAGAAAGTAAATCAGGATTTAGAAAGGTT 2000  
Db 1294 GGAGATTTAAGAAAAATTTGGAATTTAAAGAAAAAGTGTTTTTTGGACGCTCTTGAGCT 1235  
Qy 2001 AAAGATATCTTAAAGCAATTTCTAAATTTGAAGAAATTA 2040  
Db 1234 ATTGAATCTTTATAAAAATTTAAGATAAGTACTGATAGTA 1195

RESULT 7  
ID AAX20268/c  
ID AAX20268 standard; DNA; 5805 BP.  
XX AAX20268;  
AC AAX20268;  
DT 04-MAY-1999 (first entry)  
XX Borrelia burgdorferi polynucleotide sequence #21.  
DE  
XX Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
KW infection; diagnosis; characterisation; detection; ds.  
XX  
OS Borrelia burgdorferi.  
XX  
XX W09858943-A1.  
XX  
XX 30-DEC-1998.  
XX  
XX 18-JUN-1998; 98WO-US012764.  
XX  
XX 20-JUN-1997; 97US-0050359P.  
XX 22-JUL-1997; 97US-0053344P.  
XX 22-JUL-1997; 97US-0053377P.  
XX 03-SEP-1997; 97US-0057483P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (MEDI-) MEDIMUNE INC.  
XX  
XX Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
XX Smith HO;

DR WPI; 1999-081217/07.  
XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
PT products for the detection, diagnosis, characterisation, prevention and  
PT therapy of infections, particularly Lyme disease.  
XX  
XX Claim 1; Page 959-962; 1128pp; English.  
XX  
CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
CC detection, diagnosis, characterisation, prevention and therapy of Bb  
CC infections, e.g. Lyme disease. They can also be used for the production  
CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of  
CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
XX  
SQ Sequence 5805 BP; 1878 A; 1000 C; 614 G; 2290 T; 0 U; 23 Other;  
Query Match 31.5%; Score 783.8; DB 2; Length 5805;  
Best Local Similarity 82.9%; Pred. No. 4e-96;  
Matches 926; Conservative 0; Mismatches 172; Indels 19; Gaps 2;  
Qy 1 ATTTATTACACGAAACCTGACTTTTGGAGAGATTTTGAATTTATTAGAAATATGGA 60  
Db 4964 ATTTATTACAGAAATCCGATTTTAAAGAGATTTTGAATTTTATTAGAAATATGGA 4905  
Qy 61 TAATGCTAATTTGGTGTCTTTTAAACTTATGTTTGAATTTTGAATAAATAAGTACGTC 120  
Db 4904 CAATATCAATTTGGTGTATCTTTAAACTTATGTTTGTCTTTTGAATAAATAAGTACGTC 4845  
Qy 121 TTGTATCAAGATTTTCTCATTAATAATGATTTTGTGTGCTGTTTGGATAGCTCGAAT 180  
Db 4844 GCGAGTCAAGAGTTTCTTGGAAATGATTTTGAATTTTGGATAGCTCGAAT 4785  
Qy 181 CTCTGAGTGTATAACAATTTCTCTAATACAAAGTTTACATTTCTTTTTTTTGGCACAATTA 240  
Db 4784 CTCTGAGTGTATGATCAATTTCTCTAATACAAAGGTTATTTCTTTTTTTTGGCACAATTA 4725  
Qy 241 CTTTTATGTTGTATAAAGTTTTTCCATTTTGTCTTAAAAAAGTTGAATATCTTGCATTT 300  
Db 4724 CTTTAAATAGTATATAAAGTTTTTCCGGTTTTTGTCTTAAAAAAGTTGAATATCTTGCATTT 4665  
Qy 301 TTACTTTTTGCAGTTTCGGTGGCCCTGCGAGCACTTTATTCGAGTAAATGTAAAAACCAAC 360  
Db 4664 TTACTTTTTGCATTTTCAGTGCTCTACATCCATTTAAGAGTAGATGCACAAACCAAC 4605  
Qy 361 CAGATATTGGATCAGCTTGTTTAAGAGTTTGTATGATTTTCAATTTAGTTTGCATTTT 420  
Db 4604 CAGAAATTTGGGTCAATTTGTTTGGGTTTGGCACAATTTTGAATTAATTAATACATTT 4545  
Qy 421 TTGGGGTCAAAATAAATTTAGAGTTGGCTTTGAAGCTTTTGTAGTAGCTTAGAAGAAA 480  
Db 4544 TAGGGGTCAATAAATAACTTAGAGTTGGTGTGTTTGAATTTTTTTCTTAGCTTAGTGAAT 4485  
Qy 481 TTTTATAGTGA-----ATTTTAAAGAAATTTGTTTTTCATTTATTAGTT 522  
Db 4484 TTTCTAGAGATTTAAGAAATTTTATTTTCTAGAAATTTTGTTTTTTATTATGAT 4425  
Qy 523 TTTGATGATCTGTAAATTAATTTAGCATAAATCTATGTTGAAATTTTAAATTAAGAT 582  
Db 4424 TTTGATTTCTTGAAATAGTTTGGCGTAAATCCATTTGAAATTTTAAATTTAAAG 4365  
Qy 583 AATTATTGATGCCATAAAATCCCTCCTTATAAGTGTACTTTTAAATTAAGTAAAGT 642  
Db 4364 AATTATTGATGCCATAAGCAAGCTCCTTATAAGTGTACTTTTAAATTAAGTAAAGT 4305  
Qy 643 AATAAATTTGATTAATAATGTAATTTATATTATTTACCAAAACAAAAAATTTAGTCAA 702  
Db 4304 AATAAATTAGATGAAAAATGTAATTTATATTGTTACCAAAACAAAAAATTTAGTCAA 4245  
Qy 703 TTGTGTGGCTTCTCATTTGCATGCAAAATTTGGAATTTGAGTAGTGTAGTATGATAACAGAG 762

Db 4244 TTTTGTGAGTTCTCATTGTCATGCAAAATCTGGCTGTAGAGCAGGTGGGATAAACAGAA 4185  
 QY 763 AGCCAAATTTTAAGGGGTGCACCTTAAGAAAGATACATCTTTAACTGATATATAGCAAA 822  
 Db 4184 AGGCAATTTTAAAGGGGTGTACACAGAAAGATACAACTTTTGTGTATATATAGCAAA 4125  
 QY 823 GACTTTGAAATTTAAAGTTGTATGTGTTTGTAGTCTTTTATATAGCAGCGCCATTGCA 882  
 Db 4124 GACTTTGAAATTTAAATTTGTATGTGTTTGTAGTCTTTTATATAGTGTAGTGTGCA 4065  
 QY 883 ATGGAGAGATTTTAGGAGTTGATTAATAATTTATTTGGTTTTTGTATATATATATAGC 942  
 Db 4064 ATGGAGAGATTTTATGAGTTGATTAATAATTTATTTAGTTTGTGTAACAAATGTAAT-TC 4006  
 QY 943 TGAATGTAAACAAAATTTATATTTAAATCTTTGAAAAATTTGTAATTTGTTGGGTTGTGG 1002  
 Db 4005 GAAATGTAAACAAAATTTATATTTAAATCTTTGAAAAATTTGTAATTTGTTGGGTTGTGG 3946  
 QY 1003 TAAACTTAAAGCTTATGGAGTGTGATTAATAATTTATGAAATTTAAATAATGAAATTTTATTTTGTG 1062  
 Db 3945 TAAATTTGGGACTTTATGGAGTAACTTATGAAATTAAGAAATTTGAAATTTTAAATTTTGTG 3886  
 QY 1063 CTGTATTTGCTGATAGTTCTTTCGCAAGATTGATGC 1099  
 Db 3885 CAGTTTTTGTGATTAATTTCTGTGTAATAATTAATAC 3849

## RESULT 8

AAAX20280  
 ID AAAX20280 standard; DNA; 3653 BP.  
 AC AAAX20280;  
 DT  
 XX 04-MAY-1999 (first entry)  
 XX Borrelia burgdorferi polynucleotide sequence #33.  
 XX Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
 KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
 KW infection; diagnosis; characterisation; detection; ds.  
 XX  
 OS Borrelia burgdorferi.  
 XX  
 XX WO9858943-A1.  
 PN  
 XX 30-DEC-1998.  
 FD  
 XX 18-JUN-1998; 98WO-US012764.  
 XX  
 XX 20-JUN-1997; 97US-0050359P.  
 PR 22-JUL-1997; 97US-0053344P.  
 PR 22-JUL-1997; 97US-0053377P.  
 PR 03-SEP-1997; 97US-0057483P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA (MEDI-) MEDIMMUNE INC.  
 XX  
 XX Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
 PI Smith HO;  
 XX  
 DR WPI; 1999-081217/07.  
 XX  
 XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
 PT products for the detection, diagnosis, characterisation, prevention and  
 PT therapy of infections, particularly Lyme disease.  
 PT  
 XX Claim 1; Page 994-996; 1128pp; English.  
 PS  
 XX AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
 XX Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
 CC detection, diagnosis, characterisation, prevention and therapy of Bb  
 CC infections, e.g. Lyme disease. They can also be used for the production  
 CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of  
 CC

CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
 CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
 CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
 XX  
 SQ Sequence 3653 BP; 1587 A; 348 C; 690 G; 1027 T; 0 U; 1 Other;  
 Query Match 26.5%; Score 658.2; DB 2; Length 3653;  
 Best Local Similarity 70.8%; Pred. No. 2.3e-79;  
 Matches 967; Conservative 0; Mismatches 370; Indels 28; Gaps 6;  
 QY 1138 AAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAAGCAAAATATATAAGGGGAAAG 1197  
 Db 1216 AAGAAGATAAATTAAGGGGTGAGAGAAACAAATTAAGATGAATTAATCGAGGTGATG 1275  
 QY 1198 TTCAAGGATTTTGAAGAAGATTTTAGATCCAGTAAAGGATTAATAATTCCTCAATGGTC 1257  
 Db 1276 ATCCTAATAGTGGTGTAAATAATTCGTCAACAGTATTGCCAGAAATAGTCAAGATAATA 1335  
 QY 1258 CAATAGCAGATGAATTCGCAAAAATTTACAAGAAGAAAGAAAGTAAATAACGGGGAAG 1317  
 Db 1336 CACCAATATTAAAGACGCGGACAAAGTGTGTCAACAGAGAGAAAGTGAANAAG 1395  
 QY 1318 AAGAAATGATAAAGCTGTCTTTTTCAGGAGAAGATCAAAAGAGGATGAAGAGAAATAATG 1377  
 Db 1396 TAGAAGATCCGAAGCTAAAGTTGAGGGAAGAAAGAAACAAAGAGATACAGAGAAGAC 1455  
 QY 1378 AGCAAGCTGTTAATTAGAGAAATAATCGGAGAGAGATGAAGAGTTGTTAATTTAG 1437  
 Db 1456 GAAACAAACAAGATTTAGCTTAAACAAGAAGAAACAAACAAACGAAAGCAGACAG 1515  
 QY 1438 AAGAGAAAGAAATTAGAAGTTAAAAAAGAGACTGTAAGAGATGAAGATAAACAAGAAATG 1497  
 Db 1516 AAAACAAAAGAGAGAGAGCAAGAAAGACAAAAAAGAGAAAGAGAGCAAGAAAGAA 1575  
 QY 1498 AGAAACAAAACAAGAGTGGAAAAAGCACHAGAAAGAAACACACGACGACAGAGAAAGA 1557  
 Db 1576 AAGCTAAGCGCAGAAAAAGAGCTTAAGAAAGCAGAAAGCAAAAAACAAGAGAAACAAC 1635  
 QY 1558 AACGAAAAAAACAAGACAGCAAGAAAGAAACGAAACGCAAGAAACAAGAAAGAAAG 1617  
 Db 1636 AAAACGAAAGCAGAAAAAGAGAGAGAGACACGCAAGAAAGAGCGCAGAAAAAGGCAA 1694  
 QY 1618 AAAGGAGAGCTTAAACAAAAATTAACAACTTGGCGGATTAATAATAGATGAGATAAGTTGA 1677  
 Db 1695 -----GTTGATAACGAAATTTAGAACACTTACAGGCAAAATAGATCAATAGAA 1746  
 QY 1678 ATATTGATGGTATAGAAAGTCAAAACAGTGTAAACCGAAAGCAGTTTATAGATAAAATTA 1737  
 Db 1747 ATATTGATGGTATAGAGCAAACTAGTGTGGGGGCAACAGGTGTTATAGATAGAAATTA 1806  
 QY 1738 CGGGCCCTGTATATGATTATTTTACCGATGACAAACAAAAAGCTATATATAAATCATGGG 1797  
 Db 1807 CAGGSCCTGTATATGATTGATTTTACTGATG---GGAATTAAGCTATATACAAAACTTGGG 1863  
 QY 1798 GAGATTAGAGATCAAGACGCGAAGGATTCGGAATTTATTGAAAGAAATTTAGTGTATA 1857  
 Db 1864 GGGATTTCGGAAGATGATAACGACGAGGATTAGGAAGCTATTAAAGAAATTTAGTGTATA 1923  
 QY 1858 CTAGAGATGAGTTAAGAACCCAAATTTAAATAAGATTAATAAAAAATA-----TTATGCC 1911  
 Db 1924 CTAGACATAAATTAAGAACCCAAATTTAAATAGAGGTAAATAGCATATATTATTGATACTA 1983  
 QY 1912 ATGAAATGAGCTCTCTTAAAGAAATGTAGATGTCAGGGAATTAAGAGATTTAG 1971  
 Db 1984 GAAGCAGCTGAACCCCAATTTAAAGAAATGTAGGTTAGCGAAATTAATCAGACTTAG 2043  
 QY 1972 AAAAAAGTAAATTCAGGATTTAGAAAGGTTAAAGAAATATCTTTAAAGACAAATTTCTAAATTTG 2031  
 Db 2044 ATGAACTAAATCAAAATTTAGAGAGTTAAAGATATCTTTGAAAGATAAAGATAATTTTG 2103  
 QY 2032 AAGAAATTAAGGATATACATCAGTTACAGTCAG-----TAAATATATTCGATGCTTTT 2083  
 Db 2104 AAGAAATTAAGAAATACCGTTCTGCTAGTGAAGATAATTTATGATGAAGAGATTAATTTT 2163

QY 2084 AGATGTAACATAAATTTACGTACACAAAATAACAGCTAGTAGAGAAAGTTCACTGGCTGTT 2143  
DB 2164 AGATATAACATAAATTTGTATACACAAAATAACAGCTAGTA-AAAAATGACTAGTTGTT 2222  
QY 2144 ATTTTGTGTAGATTCATGTTATGAATATAGAAATGTTTCTATCAAACTTTCAATTT 2203  
DB 2223 ATTTTGTGTAGATTCATGTTATGAATATAGAAATGTTTCTATCAAACTTTCAATTT 2282  
QY 2204 AAAAAGTG-CAAAAACTATTCTAAAAATGTTGTTATTTATATATCTCTAGAGCTATG 2262  
DB 2283 AAAAATGCCAAAACATAATGCTCAAAATATGTTTATTTATATATCTCTAGAGTTATG 2342  
QY 2263 ACGTATCAATAGATTCAGATTTTGTGATGATATTTATATAGAAAAAATAAAGAA 2322  
DB 2343 ATGAATATAAATGAGATTCAGATTTTATGATAATTTATATAGAAAAAATAAAGAA 2402  
QY 2323 ATGATATAAATGAGATTCAGATTTTATTAACAGCTCTATTTAAGCTAGCCAAATCTCTAAGCAAAAAGA 2382  
DB 2403 ATGATATAAATGAGATTCAGATTTTATTAACAGCTCTATTTAAGCTAGCCAAATCTCTAAGCAAAAAGA 2462  
QY 2383 CAATNTACAGTGTCTGTGAAGAAGATCAAAAATACGTAATAAAGCCGGAAGAGTTT 2442  
DB 2463 CAATATACAGTGTCTGTGAAGAAGATCAAAAATACGTAATAAAGCCGGAAGAGTTT 2522  
QY 2443 CTTTGTAGATCGGAAGAAAGATTTGTTTAAAGACATTTGAAAGA 2487  
DB 2523 TTTTGTAGATCGGAAGAAAGATTTGTTTAAAGACATTTGAAAGA 2567

RESULT 9  
AAAX20295/c  
ID AAAX20295 standard; DNA; 2532 BP.  
XX  
AC AAAX20295;  
XX  
DT 04-MAY-1999 (first entry)  
XX  
DE Borrelia burgdorferi polynucleotide sequence #48.  
XX  
KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
KW infection; diagnosis; characterisation; detection; ds.  
XX  
OS Borrelia burgdorferi.  
XX  
PN W09858943-A1.  
XX  
PD 30-DEC-1998.  
XX  
PF 18-JUN-1998; 98WO-US012764.  
XX  
PR 20-JUN-1997; 97US-0050359P.  
PR 22-JUL-1997; 97US-0053344P.  
PR 22-JUL-1997; 97US-0053377P.  
PR 03-SEP-1997; 97US-0057483P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MEDI-) MEDIMUNE INC.  
PI Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
PI Smith HO;  
XX  
DR WPI; 1999-081217/07.  
XX  
PT New isolated Borrelia burgdorferi nucleic acids - used to develop  
PT products for the detection, diagnosis, characterisation, prevention and  
PT therapy of infections, particularly Lyme disease.  
XX  
PS Claim 1; Page 1023-1024; 1128pp; English.  
XX  
CC AAAX20248 to AAAX20402 represent polynucleotide sequences isolated from  
CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the

CC detection, diagnosis, characterisation, prevention and therapy of Bb  
CC infections, e.g. Lyme disease. They can also be used for the production  
CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of  
CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
XX  
SQ Sequence 2532 BP; 874 A; 451 C; 250 G; 955 T; 0 U; 2 Other;  
Query Match 19.8%; Score 493; DB 2; Length 2532;  
Best Local Similarity 69.6%; Pred. No. 2.5e-57;  
Matches 734; Conservative 0; Mismatches 300; Indels 21; Gaps 4;  
QY 499 GAATTTTGTGTTTCAATTTATAGTTTGTGATGATCTTTGTAATAATTTAAGCATATAAATCTA 558  
DB 2532 GAATTTTATTTTCAATTTTACCACATTTTGATAATCTTGAAATAGTTTGAGCATATAAATCCA 2473  
QY 559 TCTTGAATATTTTAAATTAAGATTAATTTTCATGTCCTATAAATCCCTCTCTATAAGT 618  
DB 2472 TATTGAAATATTTTAAATTTAAATTAATTTTATATCTATATAAATCCCTCTCTATAAGT 2413  
QY 619 GTTACTTTTAAATTAAGTAAAGTAAATAAATGATTAAAAATGATTAAAAATGATTATATTTTAC 678  
DB 2412 GTTACTTTTAAATTAAGTAAAGTAAATAAATTTAATAAATAATGATTATATTTAT 2353  
QY 679 CAAAAACAAAAAATTTAGTCAAAATGTTGCTCTCTCATTCATGCAATGCAAAAATTTGGAATG 738  
DB 2352 CAAAAACCTTAAATTTTAGTCAAAATTTTGGGTGTTCTCATTCATGCAATGCGAAATTTGGGTG 2293  
QY 739 TAGGATAGCTGTGATAAAACAGAGAGGCAATTTTTTAAGGGGTGCACTTTAAGAAACATACT 798  
DB 2292 TGGAGTGGCTGTGATAAAGATAGGATTTTTTGGAGGGTGTGCGGATAAAGAACAGT 2233  
QY 799 ATACTTTTAAATTAAGTAAAGATCTTTGAAATTTAAGTTGTTATGTTTGTAGTCT 858  
DB 2232 ATACTTTTATCTAAATATATAGCAAGACTTTGAAATTTAAGTTGTTATGTTTGTAGTCT 2173  
QY 859 TTTTATAATGACAGCCCATTTGCAATGAGAGATTTTAGGGAGTTGATTAAAAATTTATTT 918  
DB 2172 TTTGTAATGAGTGGTGCATTTGCAATGAGAGATTTTGGGAGTTGGTTAAAAATTTATTT 2113  
QY 919 TCGGTTTGTGTTAATATGTAATAGCTGAATGTAACAAAAATTTATATTTTAAATCTTTGAAA 978  
DB 2112 TCGGTTTGTGTTAATATGTAATAGCTGAATGTAACAAAAATTTATATTTTAAATCTTTGAAA 2053  
QY 979 AATTGTAATGTTTGGGTTGGTGTAAACTTTAAGCTTATGAGTGGATTTATGAATAAA 1038  
DB 2052 AATTGTAATTTATTCGGTGTTCGGTTAGATTTTAAAGACTTTATGAGCAACTTTATGAATAA -- 1995  
QY 1039 AAATGAAAAATATTTATTTTGTGCTGTTATTTGCTCATTAAGTTCTTTGCAAGATTGATG 1098  
DB 1994 ---GAAAATGTTTATTTTGTGCTATTTTGTGCTGATTTTCTTTCGAGGATTTAGC 1939  
QY 1099 CAATCGTAAAGATGCAACTGTTAAAGATGCAACTGTTAAAGATGCAACTGTTAAAGATG 1158  
DB 1938 CAAAGTGGTCAAGATGTAACAAAAAGTTTGAACCAAGATTTTAAAGGAAAGTTAAGGGAT 1879  
QY 1159 CAATCGTAAAGATGCAACCAAAATATAAAGGGAAGTTTCAAGGATTTTATGAATAAA 1218  
DB 1878 TTTTATGATACAAA---AAAGAAGAGTTTGTGAGATTTTAAACCAAGCAAGCAAG 1822  
QY 1219 TTTTATGATCCAGTAAAGGATATAAATTTGCTTCAATTTGTTCAATAGCAGATGAATTTGCAA 1278  
DB 1821 TTCAACCAAGATGTAAGAAATCTATGCAAGCTGATGAGCCCTCAGAGCAGGCGCAAGATC 1762  
QY 1279 AAAATTTACAGAGCAAGAAAAAGGTAATAACGGGGAAGAGAAATGATTAAGCTGTCT 1338  
DB 1761 AAGTGGTTCAAGGTTGCTCAAGATCAAAAATTTAAAGAGAAAGAAATTTGAACAA----- 1709  
QY 1339 TTTTATGAGAGAAATCAAAAAGAGGATGAAGAAAGAAATGAGCAAGCTCTTAAATTTAGAAG 1398  
DB 1708 ---AAAATAAGAAATTAAGGATTAAGATAGAGAGTCCGATCCCTAAAAGTGTCTCTCTTA 1651

QY 1399 AAAAAATGCGAAGAGGATAGAAAGTCTGTTAATTTAGAGAGAAAGAAATTTAGAGTTA 1458  
 Db 1650 AACATATCTGATTATGAAAAGGAAATAGAGAATT--AAAGGAAAAAATCAAAGATA 1594  
 QY 1459 AAAAAAGAGCTGGAAGAGATGAAGATGAAGAAATAGAGAAACAAAAAACAAGAGTGG 1518  
 Db 1593 AAGAAAAGTTTGAAAAAGAAATTTAGAAATCCTTGAGAAAGCTTTAAATGAAAAAATAGAGA 1534  
 QY 1519 AAAAAACACAAAGAAAGAAAAACAACGACAAAGAAA 1553  
 Db 1533 AAAAAAAGAAAGAAATTTAGAAAGAGTCTCAAAAAAAA 1499

RESULT 10  
 AAX20398  
 ID AAX20398 standard; DNA; 521 BP.  
 AC AAX20398;  
 DT 04-MAY-1999 (first entry)  
 DE Borrelia burgdorferi polynucleotide sequence #151.  
 KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
 KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
 KW infection; diagnosis; characterisation; detection; ds.  
 XX Borrelia burgdorferi.  
 OS  
 FN WO9858943-A1.  
 PD 30-DEC-1998.  
 PF 18-JUN-1998; 98WO-US012764.  
 PR 20-JUN-1997; 97US-0050359P.  
 PR 22-JUL-1997; 97US-0053344P.  
 PR 22-JUL-1997; 97US-0053377P.  
 PR 03-SEP-1997; 97US-0057483P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 FA (MEDI-) MEDIMMUNE INC.  
 XX Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
 PI Smith HO;  
 XX WPI; 1999-081217/07.  
 XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
 PT products for the detection, diagnosis, characterisation, prevention and  
 PT therapy of infections, particularly Lyme disease.  
 XX  
 XX Claim 1; Page 1111-1112; 1128pp; English.  
 CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
 CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
 CC detection, diagnosis, characterisation, prevention and therapy of Bb  
 CC infections, e.g. Lyme disease. They can also be used for the production  
 CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of  
 CC motile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
 CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
 CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
 XX

QY 446 TGGCTTTGAAGCTTTTGTAGTGGCTTAGAAGAAATTTTAGTGAATTTTAGAATTTT 505  
 Db 1 TGGTTTGAAGCTTTTGTAGTGGCTTAGAAGAAATTTTAGTGAATTTTAGAATTTT 60

Query Match 16.7%; Score 415.4; DB 2; Length 521;  
 Best Local Similarity 87.3%; Pred. No. 6e-47;  
 Matches 455; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 506 GTTTTCATTATTATTTTTCATGATCTTGTAAATAATTTAGCATATAAAATCTATGTTGAA 565  
 Db 61 ATTTTCATTATTAGCCATTTTGTAAATCTTGAAATAGTTTGAGCATATAAAATCCATGTTGAA 120  
 QY 566 ATTTATTTAAATTAAGATAAATTTATTCATGTCATATAAAATCCCTCCCTTATTAAGTGTACTT 625  
 Db 121 ATTTATTTAAATTAAGATAAATTTATTTAGTGTTCATAAAATCCTCTCTTGAAGGTGTACTT 180  
 QY 626 TTAATTTAAGTAAAAAGTAAATAAAATTTGATTAATAAATGTAATTTATTTTACCAAAAC 685  
 Db 181 TTAATTTAAGTAAAAAGTAAATAAAATAGATAAAATAGTAATTTATTTATTTGACCAAAAC 240  
 QY 686 AAAAAAATTTAGTCAAAATTTGTGGCTTCTCATTCATGCAATAAAATTTGGATTGTAGGATA 745  
 Db 241 GAAAAATTTAGTCAAAATTTGTGGCTTCTCATTCATGCAATAAAATTTGGATTGTAGGAG 300  
 QY 746 GCTGTGATAAAACAGAGAGGCAATTTTAAAGGGTGCACTTAAAGAAAGATACTATCTTT 805  
 Db 301 GCTGTGATAAAATAGATGGGCAATTTTCTGAGGGTGTGCGCTAAAGAAAGATACTATCTTT 360  
 QY 806 AAGTCATATATAGCAAAAGACTTTTGAAATTTAAAGTTGTATGTTTGTAGTCTTTTATAA 865  
 Db 361 AGCTAATATATAGCAAAAGACTTTTGAAATTTAAAGTTGTATGTTTGTAGTCTTTTATAA 420  
 QY 866 TGAGCAGGCCATTTTGCAATGGAGAGATTTTAGGGAGTTGATTAATAATTTATTTGCGTTT 925  
 Db 421 TGAGTGTGCAATTTTGCAATGGAGAGATTTTGGGGAGTTGTTTAAATTTATACATTTGCGTTT 480  
 QY 926 TGTTAATATGTAATAGTGTGATTAACAAATTTATATATTT 966  
 Db 481 TGTTAATATGTAACAGCTGAATGTAAACAAATTTATATTT 521

RESULT 11  
 AAX61805  
 ID AAX61805 standard; DNA; 1047 BP.  
 AC AAX61805;  
 DT 19-JUL-1999 (first entry)  
 DE B. burgdorferi antigenic protein coding sequence, f45-2.nt.  
 XX Antigenic protein; vaccine; Lyme disease; infection; detection; ss.  
 KW Borrelia burgdorferi.  
 OS  
 FN WO9859071-A1.  
 PD 30-DEC-1998.  
 PF 18-JUN-1998; 98WO-US012718.  
 PR 20-JUN-1997; 97US-0050359P.  
 PR 22-JUL-1997; 97US-0053344P.  
 PR 03-SEP-1997; 97US-0053748P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 FA (MEDI-) MEDIMMUNE INC.  
 XX Choi GH, Erwin AL, Hanson MS, Lathigra R;  
 XX WPI; 1999-189980/16.  
 DR P-PSDB; AAY20108.  
 XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
 PT products for the diagnosis, prevention and treatment of diseases caused  
 PT by Borrelia, particularly Lyme disease.  
 XX  
 XX Claim 1; Page 199; 275pp; English.  
 XX This sequence encodes a Borrelia burgdorferi (Bb) protein of the



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QY 1272 TTGCAAAATAATTAACAAGAGAGAAAGGTAAATAACGGGAAGAAG-----1320
Db 128 GTACAAATAATTAACAAGAGAGAAAGGTAAATAACGGGAAGAAG-----187
QY 1321 -----AAATGATAAGCTGTC 1337
Db 188 GGCAGTGGATAAATCCGCCACCAGTATTCCCGGAAAAATATTCACAATAATGCAATTAGTA 247
QY 1338 TTTTGTAGGAGAAGTAATCAAAAGAGAGATCAAGAAAGAA-----ATGAGCAAGCTGTT 1388
Db 248 TTAAGCAATAGACCAAGTGTGCTCAACAAGAAAAAAGAGAGAGAGCTGAAGCT 307
QY 1389 AATTAGAGAAAAAATCGGAGAGAGATGAAGAGTTGTTAATTTAGAGAGAAAGAA 1448
Db 308 AAAGTTGAAGAAAAATAAGAAAAACCAAGAGATACAGAGAAACATTAAAGAAAAAGAA 367
QY 1449 TTAGAAGTTAAAAAGAGAGCTGAAGAGATGAAGATAAAGAGAAATAGAGAAACAAAA 1508
Db 368 ATATAGACGACCAACCAACACAGAGATTAGCTTAAGCTTAAGAGAGAAACCAAAAA 427
QY 1509 CAAGAAGTGGAAAAAGCACAGAAAGAAAAACACGACAAAGAAAGAAACGAAAAAA 1568
Db 428 GAACAAAAAGAGATCAAGAGAGAGCAACAAAGAAAAAGCTAAAGCAGAAAAAGAAAA 487
QY 1569 CAAGACAGCAAGAGAAAGAACGAAACGACAGCAAGCAAGAAAGAAAGAGAGAGCT 1628
Db 488 GAAGAGAGAGGAGAGCAACCAACAAACGACAAAGAGAGAGAAAGAAAGGCAAGTT 547
QY 1629 AAAAAACAAATTAATAAATCTGGGATAATAGATGAGATAGTTGGAAATTTGATGCT 1688
Db 548 GATAACCAATTAATAACATATAGCTTAATAGATGAGATCAATGAAATATTGATGTT 607
QY 1689 ATAGAAAGTCAACAGAGTGAACCGAAGAGAGTTATAGATTAATTTAGGGGCTGTA 1748
Db 608 ATAAATGGCAACAGCTGTAGGCCCAAGAGGCTTTATAGATAGAAATTTAGGGGCTGTG 667
QY 1749 TATGATTATTTTCCGATGACAAACAAAGAGCTATATATAAACATGCGGAGATTAGAA 1808
Db 668 TATGATGATTTTACCAATGCAATATTTATACGCGAACTTGGAGAGGTTAGAGAG 727
QY 1809 GATGAAGAGCGAGAGATTGGGAAATATTATGAAGAAATTTAGTGAATCTAGAGATGAG 1868
Db 728 GAATCAGAGACGAGAGATTAGGAAATATTATGAAGAAATTTAGTGAATCTAGGAGCGG 787
QY 1869 TTAAGAACCAATTAATAAGAGATAATAAAATATTATGCCCATGAAATGAGCTCTCT 1928
Db 788 CTAGAACTAATTAATGAGGCAATTAACCATATCTGTTACGAA--GAGCCTAAG 844
QY 1929 CTAAGAGAAATCTAGATGTCACGGAATTTAAGAGAGATTAGAAAAAGTAAAAATCAGGA 1988
Db 845 TTAAGAGAAATCTAAGTGTAGCGAAATTTAAGAGAGATTAGAAAAATTAATTAACAA 904
QY 1989 TTAGAAAGGTTAAGAGATATCTTAAGACATTTCTAATTTTGAAGAAATTAAGGATAC 2048
Db 905 TTAGAGAGATTAAAAATATCTTAAGATAGTTCTTAATTTTGAAGAAATTAAGGATAC 964
QY 2049 ATCAGTTACAGTCAG 2063
Db 965 ATCAGTGACAGTCAG 979
```

## RESULT 13

AA61812  
ID AAX61812 standard; DNA; 1039 BP.

AC AAX61812;

XX 19-JUL-1999 (first entry)

XX B. burgdorferi antigenic protein coding sequence, t5-14.nt.

XX Antigenic protein; vaccine; Lyme disease; infection; detection; ss.

```
XX OS Borrelia burgdorferi.
XX PN WO9859071-A1.
XX PD 30-DEC-1998.
XX PF 18-JUN-1998; 98WO-US012718.
XX PR 20-JUN-1997; 97US-0050359P.
XX PR 22-JUL-1997; 97US-0053344P.
XX PR 22-JUL-1997; 97US-0053377P.
XX PR 03-SEP-1997; 97US-0057483P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (MEDI-) MEDIMMUNE INC.
XX PI Choi GH, Erwin AL, Hanson MS, Lathigra R;
XX WPI; 1999-189980/16.
XX DR P-PSDB; AAY20115.
XX PT New isolated Borrelia burgdorferi nucleic acids - used to develop
XX PT products for the diagnosis, prevention and treatment of diseases caused
XX PT by Borrelia, particularly Lyme disease.
XX PS Claim 1; Page 202; 275pp; English.
XX CC This sequence encodes a Borrelia burgdorferi (Bb) protein of the
XX CC invention, which is suitable for use in a vaccine. The Bb polypeptides
XX CC can be used in vaccines for eliciting protective antibodies to members of
XX CC the Borrelia genus, particularly for the use against Lyme disease in
XX CC humans and animals. They can be used for preventing or attenuating an
XX CC infection caused by a member of the Borrelia genus. The products can also
XX CC be used for detection of members of the Borrelia genus
XX SQ Sequence 1039 BP; 526 A; 94 C; 212 G; 207 T; 0 U; 0 Other;
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Query March 15, 58; Score 385.4; DB 2; Length 1039;

Best Local Similarity 63.58; Pred. No. 5.9e-43; Mismatches 346; Indels 3; Gaps 1;

Matches 606; Conservative 0;

QY 1113 GCACACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGAT 1172

Db 86 GCAAAAGATAAATTAATCTCAAGTAGTTCAAAAGTAGATGAATAGCAAAAAAATTACAA 145

QY 1173 GCAGACAAATATATAAGGGAAGTTCAAGGATTTTGAAGAGATTTTAGATCCAGTA 1232

Db 146 GAAGAAGATGAAGATAATGAATTAATCGGGCGATGATCCTAATACAGAGCAATAGCA 205

QY 1233 AAGGATAAATTTGTTCAAAATGGTCCAAATAGCAGATGAATTTGCAAAAAAATTACAGAA 1292

Db 206 CTGTTACCAGTATTGCCGGAATATAGTCATGCAATCCACCAGTACCAGAAAGTAAAGCA 265

QY 1293 GAAGAAAGGTAATAACGGGGAAGAGAAATGATAAGCTGCTTTTACGAGAGAA 1352

Db 266 GCACGCAAAAGTGGTGTCTCAACAAAGAGAGCCAAAAAGCAAAAGTAATAAGTT 325

QY 1353 TCAAAAGAGGATGAAGAGAAATTTAGCAAGCTGTTAATTTAGAGAAAAAATGCGGAA 1412

Db 326 GAGGAAGAAAGAGAGTTGTAGAGGAGAAAGAGAGACAGATAGTAAAAAGAAAA 385

QY 1413 GAGGATAAGAAAGTTGTTAATTTTAGAGAGAAAGATTTAGAGTTAAAAAGAGACTGAA 1472

Db 386 GTGAGAGAGCAAGCTCAAAAGAGCAAAAAAGAGAGAGAGAACTCTAAGAGAACACAA 445

QY 1473 GNACATGAAGATAAGAGAAATAGAGAAACAAAAACAAAGTGGAAAAAGCACAAGAA 1532

Db 446 AACAAGAGAGAGCAAAAGCTTAGCGAGTAGAGAGAGAGAGACGACTTAACACACAA 505

QY 1533 AGAAAAACACGACAGAGAGAAAGAAACGAAAAAAGAAACAGAGAGAGAGAGAGAA 1592

Db 506 GAACAAAAAGAGACAAACAGAGAGAGAGCTAGGTTTAAAGAGCAAAAAAGAAAAACAAGAA 565



QY 2013 AAAGACAATTCTAAATTTGAAGAAATTAAGGATACATCAGTTACAGTCAGTAAAT 2067  
 XX AAX20260/c  
 DB 1066 GAAAATGAAGATAATTTTGAAGAAATTAAGGATACATTTGAGGATAGTAATTCAT 1120

RESULT 15  
 ID AAX20260 standard; DNA; 9542 BP.  
 AC AAX20260;  
 XX  
 DT 04-MAY-1999 (first entry)  
 XX  
 DE Borrelia burgdorferi polynucleotide sequence #13.  
 XX  
 KW Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;  
 KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;  
 KW infection; diagnosis; characterisation; detection; ds.  
 XX  
 OS Borrelia burgdorferi.  
 XX  
 XX WO9858943-A1.  
 XX  
 XX 30-DEC-1998.  
 XX  
 XX 18-JUN-1998; 98WO-US012764.  
 XX  
 XX 20-JUN-1997; 97US-0050359P.  
 XX  
 XX 22-JUL-1997; 97US-0053344P.  
 XX  
 XX 22-JUL-1997; 97US-0053377P.  
 XX  
 XX 03-SEP-1997; 97US-0057483P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX (MEDI-) MEDIMUNE INC.  
 XX  
 XX Fraser C, White OR, Clayton R, Dougherty BA, Lathigra R;  
 XX Smith HO;  
 XX WPI; 1999-081217/07.  
 XX  
 XX New isolated Borrelia burgdorferi nucleic acids - used to develop  
 XX products for the detection, diagnosis, characterisation, prevention and  
 XX therapy of infections, particularly Lyme disease.  
 XX  
 XX Claim 1; Page 920-925; 1128pp; English.

CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from  
 CC Borrelia burgdorferi (Bb). Products derived from Bb can be used for the  
 CC detection, diagnosis, characterisation, prevention and therapy of Bb  
 CC infections, e.g. Lyme disease. They can also be used for the production  
 CC of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of  
 CC mobile, spiral-shaped bacteria called Spirochetes. Spirochetes are  
 CC pathogenic in humans and Borrelia causes epidemic and endemic relapsing  
 CC fever, and Lyme borreliosis, more commonly known as Lyme disease  
 XX  
 XX Sequence 9542 BP; 3812 A; 1160 C; 1113 G; 3457 T; 0 U; 0 Other;  
 SQ

Query Match 13.5%; Score 336.8; DB 2; Length 9542;  
 Best Local Similarity 68.6%; Pred. No. 1.6e-36;  
 Matches 520; Conservative 0; Mismatches 212; Indels 26; Gaps 3;  
 1 ATTATTATACAGAACCCCTGACCTTTTGAGAGATTGTAATTTATTTAGAAATATGGA 60  
 4722 ATTTACGTCGCTTCAAAACCCCAATTTCTAAGTAACCTTTTGAATTTTATGCAATCAGT 4663  
 61 TAATGCTAATTTGCTTGTCTTAACTATGTTTGAATTTTGAAGAAATTAAGTACGTC 120  
 4662 CAATGCTAATTTGATATATCTTTAAACCTAATGTTTGGTTTGTGAAGAAATTAAGTACGTC 4603  
 121 TTGATACAGATTTTCTCATTAATGATTTTGTGCTGCTGTTGATAGCTCGAAT 180  
 4602 TAGTATTAAAGATTTTCTTTTGAAGTAAATTTGCTGCTACTTTTGAATAGCAATTAAT 4543

QY 181 CTTCGAGTTGATACAAATTTCTCTAATACAACTTACATTTCTTTTTCGCCACATTTA 240  
 DB 4542 CTTTTCGGTTATAACAAATTCCTCTAGTACAACTAGTAATTTTTCCTTTCGCCACATTTA 4483  
 QY 241 CTTTATATGTTGATAAAAGTTTTCCTATTTTTCCTTAAAAAGTTGAAATATCTTGCATTT 300  
 DB 4482 CTTTATATGTTGATAAAAGTTTTCCTATTTTTCCTTAAAAAGTTGAAATATCTTGCATTT 4423  
 QY 301 TTACTTTTTCAGTTTCGGTCCCTCGAGCCACTTATTCGAGTAATGTAAGAAACCAAC 360  
 DB 4422 TTACTTTTTCAGTTTCGGTCCCTCGAGCCACTTATTCGAGTAATGTAAGAAACCAAC 4363  
 QY 361 CAGATATTGGATCAGCTTGTGTTAAGAGTTTGTGATGCAATTTTCAATTTAGTTTGCCTAATTT 420  
 DB 4362 CAGCTATTGGTCAATTTGTTTAAATGCTTTGACACATTTTATAATTAATTTGATTAGTTT 4303  
 QY 421 TTGGGTCAAATAAAATTTAGGAGTTGGCTTTTGAAGCTTT-----TTTAGTAG 468  
 DB 4302 TTGGATTTAAGTACACACTTAGCAGTGGTTTTTAGAATTTTCTGTTTATTTCTTTTAT 4243  
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 DB 4062 AATAAATAATTAATTAATTTATTTATTTATTTCTATGTCATAGTTTCTATGATATCAAAAAAT 4003  
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 DB 4002 CACTAAAAATTTTGAGATTATTGTTGTTATTTAATTT 3965

Search completed: July 29, 2004, 16:32:51  
 Job time : 993 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: July 29, 2004, 15:00:53 ; Search time 9526 Seconds  
(without alignments)  
11315.781 Million cell updates/sec  
Title: US-09-830-228-51  
Perfect score: 2487  
Sequence: 1 ATTATTATACGAGAACCCCT.....TTAAGACACTTTGAAAGA 2487

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

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- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
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- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_vrt.\*
- 37: em\_htg\_mam.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2485	99.9	52971	1	AE001584	AE001584 Borrelia
2	1424.4	57.3	1426	1	AF020657	AF020657 Borrelia
3	1149.6	46.2	5108	1	BU44914	BU44914 Borrelia bu
4	1088	43.7	3468	1	AF077603	AF077603 Borrelia
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6	990	38.8	3662	1	BU18292	BU18292 Borrelia bu
7	970	33.0	30885	1	AE001580	AE001580 Borrelia
8	966.8	38.9	30750	1	AE001575	AE001575 Borrelia
9	963.8	38.8	8942	1	AF023853	AF023853 Borrelia
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13	875.6	35.2	4283	1	BU44912	BU44912 Borrelia bu
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15	873	35.1	3904	1	BU42598	BU42598 Borrelia bu
16	873	35.1	30223	1	AE001576	AE001576 Borrelia
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21	772.8	31.1	2849	1	BU44913	BU44913 Borrelia bu
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ALIGNMENTS

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LOCUS AE001584 52971 bp DNA linear BCT 17-MAR-2003  
DEFINITION Borrelia burgdorferi B31 plasmid lp56, complete plasmid sequence.  
ACCESSION AE001584  
VERSION AE001584.1 GI:6382393  
KEYWORDS  
SOURCE Borrelia burgdorferi B31  
ORGANISM Borrelia burgdorferi B31  
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
Borrelia burgdorferi group.  
1 (bases 1 to 52971)  
REFERENCE  
AUTHORS Casjens, S., Palmer, N., van Vugt, R., Huang, W.M., Stevenson, B.,  
Rosa, P., Lathigra, R., Sutton, G., Peterson, J., Dodson, R.J., Hatt, D.,  
Hickey, E., Gwinn, M., White, O. and Fraser, C.M.



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RESULT 2

AF020657

LOCUS

DEFINITION *Borrelia burgdorferi* plasmid lp56 *ErpX* protein (*erpX*) gene, linear BCT 03-JUN-1998

complete cds.  
 AF020657  
 AF020657.1 GI:2444427  
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 SOURCE  
 ORGANISM  
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 Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*;  
*Borrelia burgdorferi* group.  
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*Borrelia burgdorferi* *erp* proteins are immunogenic in mammals  
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 Infect. Immun. 66 (6), 2648-2654 (1998)  
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 PUBMED  
 9596729  
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## ORIGIN

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 ACCESSION  
 U44914  
 VERSION  
 U44914.1  
 GI:3559777  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
 Borrelia burgdorferi group.  
 REFERENCE  
 1 (bases 1 to 5108)  
 Stevenson, B., Tilly, K. and Rosa, P.A.  
 A family of genes located on four separate 32-kilobase circular  
 plasmids in Borrelia burgdorferi B31  
 J. Bacteriol. 178 (12), 3508-3516 (1996)  
 REFERENCE  
 2 (bases 1 to 5108)  
 Casjens, S., van Vugt, R., Tilly, K., Rosa, P.A. and Stevenson, B.  
 Homology throughout the multiple 32-kilobase circular plasmids  
 present in Lyme disease spirochetes  
 J. Bacteriol. 179 (1), 217-227 (1997)  
 REFERENCE  
 3 (bases 1 to 5108)  
 Stevenson, B., Tilly, K. and Rosa, P.A.  
 Direct Submission  
 Submitted (10-JAN-1996) Brian Stevenson, Rocky Mountain Labs,  
 NIAID, NIH, 903 South 4th St., Hamilton, MT 59840, USA  
 REFERENCE  
 4 (bases 1 to 5108)  
 Stevenson, B.  
 Direct Submission  
 Submitted (09-SEP-1998) Microbiology & Immunology, Univ. Kentucky,  
 800 Rose St. Lexington, KY 40536, USA  
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 Sequence update by submitter  
 On Sep 9, 1998 this sequence version replaced gi:1675212.  
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RESULT 4  
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DEFINITION Borrelia burgdorferi strain 297 plasmid-encoded ElpA2 protein  
ACCESSION AF077603  
VERSION AF077603.1 GI:4704437  
KEYWORDS  
SOURCE Borrelia burgdorferi (Lyme disease spirochete)  
ORGANISM Borrelia burgdorferi  
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
Borrelia burgdorferi group.  
REFERENCE 1 (bases 1 to 3468)  
AUTHORS Akins,D.R., Caimano,M.J., Yang,X., Cerna,F., Norgard,M.V. and Radolf,J.D.  
TITLE Molecular and evolutionary analysis of Borrelia burgdorferi 297 circular plasmid-encoded lipoproteins with OspE- and OspF-like leader peptides  
JOURNAL Infect. Immun. 67 (3), 1526-1532 (1999)  
MEDLINE 99150296  
PUBMED 10024606  
REFERENCE 2 (bases 1 to 3468)  
AUTHORS Norgard,M.V. and Radolf,J.D.  
TITLE Direct Submission  
JOURNAL Submitted (11-JUL-1998) Internal Medicine, UT Southwestern Med. School, 5323 Harry Hines Blvd., Dallas, TX 75235, USA  
FEATURES  
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LOCUS Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds.

DEFINITION U42599

ACCESSION U42599

VERSION U42599.1 GI:2182753

KEYWORDS

SOURCE Borrelia burgdorferi (Lyme disease spirochete)

ORGANISM Borrelia burgdorferi

REFERENCE 1 (bases 1 to 5579)

AUTHORS Stevenson,B., Casjens,S., van Vugt,R., Porcella,S.F., Tilly,K., Bono,J.L., and Rosa,P.

TITLE Characterization of cp18, a naturally truncated member of the cp32 family of Borrelia burgdorferi plasmids

JOURNAL J. Bacteriol. 179 (13), 4285-4291 (1997)

MEDLINE 97352686

PUBMED 920945

REFERENCE 2 (bases 1 to 5579)

AUTHORS Stevenson,B., Casjens,S., van Vugt,R., Porcella,S.F., Tilly,K., Bono,J.L., and Rosa,P.

TITLE Characterization of cp18, a naturally truncated member of the cp32 family of Borrelia burgdorferi plasmids

JOURNAL J. Bacteriol. 179 (13), 4285-4291 (1997)

MEDLINE 97352686

PUBMED 920945

REFERENCE 3 (bases 1 to 5579)

AUTHORS Stevenson,B., Tilly,K. and Rosa,P.A.

TITLE Direct Submission

JOURNAL Submitted (08-DEC-1995) Brian Stevenson, Rocky Mountain Labs,

NIAID, NIH, 903 South 4th St., Hamilton, MT 59840, USA

On Jun 11, 1997 this sequence version replaced gi:1373120.

Location/Qualifiers

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Borrelia burgdorferi BbK2.10 precursor (bbk2.10) and BapA genes,
complete cds; and unknown genes.
U18292
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Borrelia burgdorferi (Lyme disease spirochete)
Borrelia burgdorferi
Borrelia burgdorferi
Borrelia burgdorferi group.
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Akins,D.R., Porcella,S.F., Popova,T.G., Shevchenko,D., Baker,S.I.,
Li,M., Norgard,M.V. and Radolf,J.D.
Evidence for in vivo but not in vitro expression of a Borrelia
burgdorferi outer surface protein F (OspF) homologue
Mol. Microbiol. 18 (3), 507-520 (1995)
96342380
8748034
2 (bases 1 to 3662)
Akins,D.R.
Direct Submission
Submitted (07-DEC-1994) Darrin R. Akins, Molecular Microbiology, UT
Southwestern Med. School at Dallas, 5323 Harry Hines Blvd., Dallas,
TX 75235-9048, USA
3 (bases 1 to 3662)
Akins,D.R.
Direct Submission
Submitted (13-JUL-1998) Darrin R. Akins, Molecular Microbiology, UT
Southwestern Med. School at Dallas, 5323 Harry Hines Blvd., Dallas,
TX 75235-9048, USA
Sequence update by submitter
On Jul 13, 1998 this sequence version replaced gi:1052863.
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Best Local Similarity 64.0%; Pred. No. 8.9e-98;
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Db	25834	TTTTAGTGAATTTTAAAGAAATTTTATTTTCAATTTAGCAATTTTGATAATCTTGAAATA	25893	26914	TATAGGAGAGCGGTATATGAATATAAAAAACAATTTATTTTGTGCAGTTTTCGCCTGA	26973
Qy	541	ATTAAAGCATAAATCTATGTTGGAATTTTAAATTTAAATTAAGATAATTTATTCATGTCCTATAA	600	1147	-----CTGGTAAAGATGCAACTGGTAAAAATCGAGAACAAAAATATAAAAGGGAAGTTTC	1200
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Qy	601	AATCCCTCCTTTAAAGTGTACTTTTAAATTAAGTAAAGTAAATTAATAATTTGATTAATA	660	1201	AAGGATTTTGTAGAAAAGATTTTATAGTCCAGTAAAGATTAATTTGCTTCAATTTGCTCCAA	1260
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Qy	721	CATGCAAAATTTGGATTTAGGATAGCTGTGATAAAACAGAGAGGCAATTTTAAAGGGGT	780	1321	AAAAAT-----	1325
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DEFINITION Borrelia burgdorferi B31 plasmid cp32-1, complete plasmid sequence.  
ACCESSION AE001575  
VERSION AE001575.1 GI:6382081  
KEYWORDS  
SOURCE Borrelia burgdorferi B31  
ORGANISM Borrelia burgdorferi B31  
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
Borrelia burgdorferi group.  
REFERENCE 1 (bases 1 to 30750)  
Casjens,S., Palmer,N., van Vugt,R., Huang,W.M., Stevenson,B.,  
Rosa,P., Lathigra,R., Sutton,G., Peterson,J., Dodson,R.J., Haft,D.,  
Hickey,E., Gwinn,M., White,O., and Fraser,C.M.  
A bacterial genome in flux: the twelve linear and nine circular  
extrachromosomal DNAs in an infectious isolate of the Lyme disease  
spirochete Borrelia burgdorferi  
Mol. Microbiol. 35 (3), 490-516 (2000)  
20138354  
MEDLINE 10672174  
PUBMED  
REFERENCE 2 (bases 1 to 30750)  
Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Lathigra,R.,  
White,O., Dodson,R., Hickey,E.K., Gwinn,M., Peterson,J.,  
van-Vugt,R., Palmer,N., Haft,D., Rosa,P. and Stevenson,B.  
Direct Submission  
Submitted (11-NOV-1999) The Institute for Genomic Research, 9712  
Medical Center Dr, Rockville, MD 20850, USA  
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QY	841	GTATGCTTTTGTAGTCTTTTATATATAGCAGGCCATTTCCAAATGAGAGATTTTAGGGA	900
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Db	26659	ATACTGAATATATTACATTTTATAGGATTAATTAATACAGTGGGGGGAGACAAA	26718
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Db	28095	TATATCTCTCTAGAGTTATGATGAATATAAATGAGATTTTCCAGATTTTGTATGATAATTTA	28154
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RESULT 10
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DEFINITION Borrelia burgdorferi B31 plasmid cp32-9, complete plasmid sequence.
ACCESSION AE001581
VERSION   AE001581.1 GI:6382346
KEYWORDS
SOURCE    Borrelia burgdorferi B31
ORGANISM  Borrelia burgdorferi B31
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           Borrelia burgdorferi group.
REFERENCE  1 (bases 1 to 30651)
AUTHORS   Casjens,S., Palmer,N., van Vugt,R., Huang,W.M., Stevenson,B.,
           Rosa,P., Lathigra,R., Sutton,G., Peterson,J., Dodson,R.J., Haft,D.,
           Hickey,E., Gwinn,M., White,O. and Fraser,C.M.
           A bacterial genome in flux: the twelve linear and nine circular
           extrachromosomal DNAs in an infectious isolate of the Lyme disease
           spirochete Borrelia burgdorferi
           Mol. Microbiol. 35 (3), 490-516 (2000)
JOURNAL   20138354
MEDLINE   10672174
PUBMED    2 (bases 1 to 30651)
AUTHORS   Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Lathigra,R.,
           White,O., Dodson,R., Hickey,E.K., Gwinn,M., Peterson,J.,
           van-Vugt,R., Palmer,N., Haft,D., Rosa,P. and Stevenson,B.
           Direct Submission
           Submitted (11-NOV-1999) The Institute for Genomic Research, 9712
           Medical Center Dr, Rockville, MD 20850, USA
JOURNAL   3 (bases 1 to 30651)
AUTHORS   Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Lathigra,R.,
           White,O., Dodson,R., Hickey,E.K., Gwinn,M., Peterson,J.,
           van-Vugt,R., Palmer,N., Haft,D., Rosa,P. and Stevenson,B.
           Direct Submission
           Submitted (21-JUN-2002) The Institute for Genomic Research, 9712
           Medical Center Dr, Rockville, MD 20850, USA
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AUTHORS Casjens, S., Palmer, N., van Vugt, R., Huang, W.M., Stevenson, B.,  
Rosa, P., Lathigra, R., Sutton, G., Peterson, J., Dodson, R.J., Haft, D.,  
Hickey, E., Gwinn, M., White, O. and Fraser, C.M.  
A bacterial genome in flux: the twelve linear and nine circular  
extrachromosomal DNAs in an infectious isolate of the Lyme disease  
spirochete Borrelia burgdorferi  
JOURNAL Mol. Microbiol. 35 (3), 490-516 (2000)  
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AUTHORS Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Lathigra, R.,  
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VERSION U30617.1 GT:3309515  
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ORGANISM Borrelia burgdorferi  
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
Borrelia burgdorferi group.  
REFERENCE 1 (bases 1 to 3231)  
AUTHORS Akins,D.R., Porcella,S.F., Popova,T.G., Shevchenko,D., Baker,S.I.,  
Li,M., Norgard,M.V. and Radolf,J.D.  
TITLE Evidence for in vivo but not in vitro expression of a Borrelia  
burgdorferi outer surface protein F (OspF) homologue  
JOURNAL Mol. Microbiol. 18 (3), 507-520 (1995)  
MEDLINE 96342380  
PubMed 8748034  
REFERENCE 2 (bases 1 to 3231)  
AUTHORS Akins,D.R.  
TITLE Direct Submission

JOURNAL Submitted (29-JUN-1995) Darrin R. Akins, UT Southwestern Med.  
School at Dallas, Molecular Microbiology, 5323 Harry Hines Blvd.,  
Dallas, TX 75235-9048, USA  
REFERENCE 3 (bases 1 to 3231)  
AUTHORS Akins,D.R.  
TITLE Direct Submission  
JOURNAL Submitted (13-JUL-1998) Darrin R. Akins, UT Southwestern Med.  
School at Dallas, Molecular Microbiology, 5323 Harry Hines Blvd.,  
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## RESULT 13

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ACCESSION  
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VERSION  
U4912.1 GI:3559781  
KEYWORDS  
SOURCE  
ORGANISM  
Borrelia burgdorferi (Lyme disease spirochete)  
Borrelia burgdorferi  
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
Borrelia burgdorferi group.  
REFERENCE  
1 (bases 1 to 4283)  
Stevenson, B., Tilly, K. and Rosa, P. A.  
A family of genes located on four separate 32-kilobase circular plasmids in Borrelia burgdorferi B31  
J. Bacteriol. 178 (12), 3508-3516 (1996)  
96256604  
PUBMED  
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REFERENCE  
2 (bases 1 to 4283)  
Casjens, S., van Vleet, R., Tilly, K., Rosa, P. A. and Stevenson, B.  
Homology throughout the multiple 32-kilobase circular plasmids present in Lyme disease spirochetes  
J. Bacteriol. 179 (1), 217-227 (1997)  
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REFERENCE  
3 (bases 1 to 4283)  
Stevenson, B., Tilly, K. and Rosa, P. A.  
Direct Submission  
Submitted (10-JAN-1996) Brian Stevenson, Rocky Mountain Labs, NIAID, NIH, 903 South 4th St., Hamilton, MI 59840, USA  
JOURNAL  
TITLE  
REFERENCE  
4 (bases 1 to 4283)  
Stevenson, B.  
Direct Submission  
Submitted (09-SEP-1998) Microbiology & Immunology, Univ. Kentucky, 800 Rose St., Lexington, KY 40536, USA  
JOURNAL

## ORIGIN

Query Match 35.2%; Score 875.6; DB 1; Length 4283;  
Best Local Similarity 65.4%; Pred. No. 3.5e-87;



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Qy	1788	AAACATGGGGAGATTTTAGAAGATGAAGAGCGCAGGATGGGAAAAATTTTGAAGAA	1847
Db	3175	AGTTTAAAGTCAAAATATAGAGAAATTTATACAGAACTAAAAAGAGCTTTTCTAAAGAA	3234
Qy	1848	TTGATGATACCTAGAGATGAGTTAAGAACCAAAATTAATTAAGATTAATAAAAAATTTAT	1907
Db	3235	GATTTTAACTTAATAATAAGACTAGATAATTATGATTTTAAATGAGTATGAATA	3294
Qy	1908	GCCATGAAATGAGCCTCCTCTAAAGAAATGTAGATGTCAGCGAAATTTAAAGAGAT	1967
Db	3295	AGTCATGTTTTTCCGATGCTCCTAGAAATTAGAGGAGATTAAAGAAAAATTTGGAATAAA	3354
Qy	1968	TTAGAAAGTAAATCAGGATTAGAAAGTTAAAGAAATATCTTAAAGCAATTTCTATA	2027
Db	3355	GAAAAAGTGTTTTTTTGGAGGCTCTTGAGGCTATTGATATCTTTATAAAATTAAGATA	3414
Qy	2028	TTTGAGAAATTA	2040
Db	3415	AGTACTGATAGTA	3427

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Job time : 9607 secs